

AD _____
(Leave blank)

Award Number:
W81XWH-08-1-0139

TITLE:
Functional Proteomic Analysis of Lipid Raft Kinase Complexes

PRINCIPAL INVESTIGATOR:
Wei Yang

CONTRACTING ORGANIZATION:
Children's Hospital
Avenue, Boston, MA 02115

REPORT DATE:
August 2009

TYPE OF REPORT:
Annual Summary

PREPARED FOR: U.S. Army Medical Research and Materiel Command
Fort Detrick, Maryland 21702-5012

DISTRIBUTION STATEMENT: (Check one)

- ☒ Approved for public release; distribution unlimited
- ☐ Distribution limited to U.S. Government agencies only;
report contains proprietary information

The views, opinions and/or findings contained in this report are those of the author(s) and should not be construed as an official Department of the Army position, policy or decision unless so designated by other documentation.

REPORT DOCUMENTATION PAGE				Form Approved OMB No. 0704-0188	
Public reporting burden for this collection of information is estimated to average 1 hour per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing this collection of information. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to Department of Defense, Washington Headquarters Services, Directorate for Information Operations and Reports (0704-0188), 1215 Jefferson Davis Highway, Suite 1204, Arlington, VA 22202-4302. Respondents should be aware that notwithstanding any other provision of law, no person shall be subject to any penalty for failing to comply with a collection of information if it does not display a currently valid OMB control number. PLEASE DO NOT RETURN YOUR FORM TO THE ABOVE ADDRESS.					
1. REPORT DATE (DD-MM-YYYY) 31/08/2009		2. REPORT TYPE Annual Summary		3. DATES COVERED (From - To) 1 Aug 2008 - 31 Jul 2009	
4. TITLE AND SUBTITLE Functional Proteomic Analysis of Lipid Raft Kinase complexes				5a. CONTRACT NUMBER W81XWH-08-0139	
				5b. GRANT NUMBER PC073281	
				5c. PROGRAM ELEMENT NUMBER	
6. AUTHOR(S) Wei Yang Email: wei.yang@childrens.harvard.edu				5d. PROJECT NUMBER	
				5e. TASK NUMBER	
				5f. WORK UNIT NUMBER	
7. PERFORMING ORGANIZATION NAME(S) AND ADDRESS(ES) Children's Hospital Boston Massachusetts 02115				8. PERFORMING ORGANIZATION REPORT NUMBER	
9. SPONSORING / MONITORING AGENCY NAME(S) AND ADDRESS(ES) U.S. Army Medical Research and Material Command Fort Detrick Maryland 21703-5012				10. SPONSOR/MONITOR'S ACRONYM(S)	
				11. SPONSOR/MONITOR'S REPORT NUMBER(S)	
12. DISTRIBUTION / AVAILABILITY STATEMENT Approved for public release; distribution unlimited					
13. SUPPLEMENTARY NOTES					
14. ABSTRACT A series of studies from our laboratories suggested that survival signaling in prostate cancer cells is mediated, in part, through lipid raft-resident Akt. I have hypothesized that the lipid raft-resident Akt in prostate tumor cells is a privileged Akt population that mediates cell survival by interacting with discrete subsets of regulatory proteins and by transmitting signals that are unique to the lipid raft environment. Many components in lipid raft-resident Akt complexes and Akt pathways are likely to be palmitoylated, given that a number of key signaling molecules are palmitoylated and that palmitoyl proteins have been proposed to be enriched in lipid rafts. As an approach into the analysis of Akt signaling through lipid rafts, in year 1 of this project I developed a novel, proteomic method of palmitoyl protein analysis, which resulted in many interesting and unanticipated biological findings. In addition, our group has very recently reported that EGF stimulation or accumulation of Akt1 in lipid rafts resulted in the rapid formation of secreted microvesicles, which are capable of activating phosphotyrosine and Akt pathway signaling as well as stimulating proliferation and migration in recipient cells. Functional palmitoylproteomics analysis suggested that certain palmitoyl proteins actively participate in transmitting EGFR-Akt signaling. The protein acyltransferases and acylprotein thioesterases regulating the palmitoylation levels of these key palmitoyl proteins may be novel targets for the inhibition of EGFR-Akt signaling, which can be exploited for the treatment of advanced prostate cancer.					
15. SUBJECT TERMS Akt; EGFR; Lipid rafts; Mass spectrometry; Palmitoylation; Prostate Cancer					
16. SECURITY CLASSIFICATION OF:			17. LIMITATION OF ABSTRACT UU	18. NUMBER OF PAGES 100	19a. NAME OF RESPONSIBLE PERSON USAMRMC
a. REPORT U	b. ABSTRACT U	c. THIS PAGE U			19b. TELEPHONE NUMBER (include area code)

Table of Contents

	<u>Page</u>
Introduction.....	3
Body.....	3
Key Research Accomplishments.....	14
Reportable Outcomes.....	14
Conclusion.....	15
References.....	15
Appendices.....	16

Introduction

The molecular mechanisms underlying the development and progression of prostate cancer (PCa), the second leading cause of cancer deaths in the United States, remain largely unknown. A series of studies from our laboratory suggested that survival signaling in prostate tumor cells is mediated, in part, through lipid raft-resident Akt (1-5). Lipid rafts are liquid-ordered membrane domains enriched with cholesterol and sphingolipids, which serve as crucial platforms for signal transduction by sequestering and excluding signaling proteins and by harboring pre-formed multiprotein signaling complexes (7). Akt is a central signaling protein that is frequently activated in PCa. I have hypothesized that the lipid raft-resident Akt in PCa cells is a privileged Akt population that mediates cell survival by interacting with discrete subsets of regulatory proteins and by transmitting signals that are unique to the lipid raft environment. Protein palmitoylation, a reversible lipid modification more accurately known as protein S-acylation, plays a critical role in modulating protein activity and stability, protein-protein interactions, and shuttling of proteins between subcellular compartments in response to changes in signal transduction (8). Given that a number of key signaling molecules are palmitoylated and that palmitoyl proteins have been proposed to be enriched in lipid rafts, some palmitoyl proteins may reside in lipid raft-resident Akt complexes and are actively involved in the lipid raft and non-raft Akt pathways. The purpose of this project is to identify palmitoyl proteins in lipid raft-resident Akt complexes and compare palmitoyl proteins involved in the lipid raft Akt pathway and the non-raft Akt pathway.

Body

In year 1, I have developed a novel method to enrich and identify palmitoyl proteins as well as characterize palmitoylation sites at the proteome scale. I have applied this method to perform global analysis of palmitoyl proteins in raft-enriched and non-raft membranes isolated from DU145 human prostate cancer cells, which resulted in many novel biological findings that, interestingly, were not anticipated when I began this project. I have started to use this method, coupled with stable isotope labeling with amino acids in cell culture (SILAC), to identify lipid raft and non-raft palmitoyl proteins transmitting EGFR signaling. I believe this novel approach will lead to the discovery of palmitoyl proteins in lipid raft-resident Akt complexes as well as those involved in the lipid raft Akt pathway and the non-raft Akt pathway. Moreover, I anticipate that these studies will result in the identification of a new class of molecular targets for anticancer therapy.

In addition to the scientific achievements, I have also made substantial progress on my training program. The one-year rigorous training in Dr. Michael Freeman's lab has greatly facilitated my transition from a proteomics specialist to a cancer researcher. The collaboration with Dr. Hanno Steen, Director of the Proteomics Center at Children's Hospital, has expedited my mastering of many sophisticated proteomics techniques, which substantially enhanced the discovery component of this project. In addition, regular attendance of cutting-edge seminars in the Longwood Medical Area and active interaction with senior scientists and clinicians have greatly broaden my knowledge and experience and facilitated my development into a productive and imaginative scientist.

1. Procedure for purification and identification of palmitoyl proteins and peptides

In cancer cells, upregulation of lipogenic pathways, is known to alter the plasma membrane in unspecified ways (9). Lipid raft-resident Akt associates with lipids and lipid-modified proteins that originate from these

upregulated lipogenic synthetic mechanisms, particularly those involving the abundant cytosolic protein, fatty acid synthase (FASN), which has been described as a metabolic oncogene and is the primary source of long-chain fatty acids in cancer cells (10,11). As an approach into the analysis of Akt signaling through lipid rafts, in year 1 of this project I developed a novel, proteomic method of palmitoyl-protein analysis, which we have begun to use to study lipid raft-dependent signaling mechanisms.

Because the commonly used ^3H -palmitate metabolic labeling method is hazardous and time-consuming, two complementary methods have been developed previously to detect and/or purify palmitoyl proteins at the proteome scale. One method involves the metabolic incorporation of an azide- or alkyne-containing palmitate analogue into proteins (12-14). The azido/alkynyl groups, which are metabolically inert in cellular environments, can be specifically and efficiently conjugated with a tag (*e.g.*, biotin, Myc, and fluorescein) by chemoselective ligations (*e.g.*, Staudinger reaction and azide-alkyne [3+2] cycloaddition reaction) *in vitro*. Consequently, palmitoyl proteins containing the azide/alkyne moiety can be detected and/or purified with minimal contamination. The second method, named acyl-biotinyl exchange (ABE) (15-18), has been more widely used than the palmitate analogue metabolic labeling method. In this approach, thioester bonds are selectively cleaved by neutral hydroxylamine (HA) and palmitoyl moieties are replaced by biotinyl groups. Consequently, palmitoyl proteins can be detected and/or purified via streptavidin-biotin interactions. Unlike the palmitate analogue labeling method, the ABE approach can be readily applied to analyze tissue samples and cancer cells because no metabolic labeling is required. Therefore, I adopted the ABE approach and optimized a protocol developed by Davis and coworkers (16) so that palmitoyl proteins can be enriched with minimal contamination and palmitoylation sites can be characterized. I named this new method PalmPISC (palmitoyl protein identification and site characterization).

As shown in the upper part of Figure 1, the palmitoyl groups are replaced with biotinyl groups using the ABE method prior to palmitoyl protein/peptide purification. Thioester bonds were broken by TCEP, a potent reducing agent that does not cleave thioester bonds. All free thiol groups were irreversibly blocked by N-ethylmaleimide (NEM), a widely used alkylating agent. Total TCEP-reduced and NEM-alkylated proteins were equally divided into two portions: one was treated with neutral HA to specifically cleave off palmitoyl moieties and the other was not treated with HA (not shown). Subsequently, newly formed thiols were labeled with biotin-HPDP.

As shown in the lower left part of Figure 1, *in vitro* biotinylated (formerly palmitoylated) proteins were enriched by streptavidin affinity chromatography and gently eluted by TCEP, leaving endogenous biotinylated proteins and nonspecifically bound proteins on the streptavidin-agarose beads. Enriched proteins were separated by SDS-PAGE, followed by in-gel digestion and LC-MS/MS analysis. Subsequently, a label-free quantification method called spectral counting (19) was applied to distinguish palmitoyl proteins from contaminating proteins. Notably, prior to tryptic digestion, the free thiols (potentially formerly palmitoylated) were blocked by iodoacetamide so that the palmitoylation sites, which were eventually carbamidomethylated, can be distinguished from nonpalmitoylated cysteines, which were blocked by NEM prior to the ABE reaction.

However, due to the low stoichiometry of palmitoylation, the protein-based procedure only led to the characterization of a small number of palmitoylation sites. Therefore, a peptide-based procedure (Fig. 1,

lower right part) was developed to enrich palmitoyl peptides so that more palmitoylation sites can be localized. After ABE chemical reactions (Fig. 1, upper part), whole protein lysates were digested in solution prior to affinity purification. *In vitro* biotinylated (previously palmitoylated) peptides were selectively enriched by streptavidin affinity chromatography. Bound peptides were gently eluted by TCEP and originally palmitoylated cysteine residues became free cysteines. In contrast, nonpalmitoylated cysteines were irreversibly blocked by NEM in a previous step.

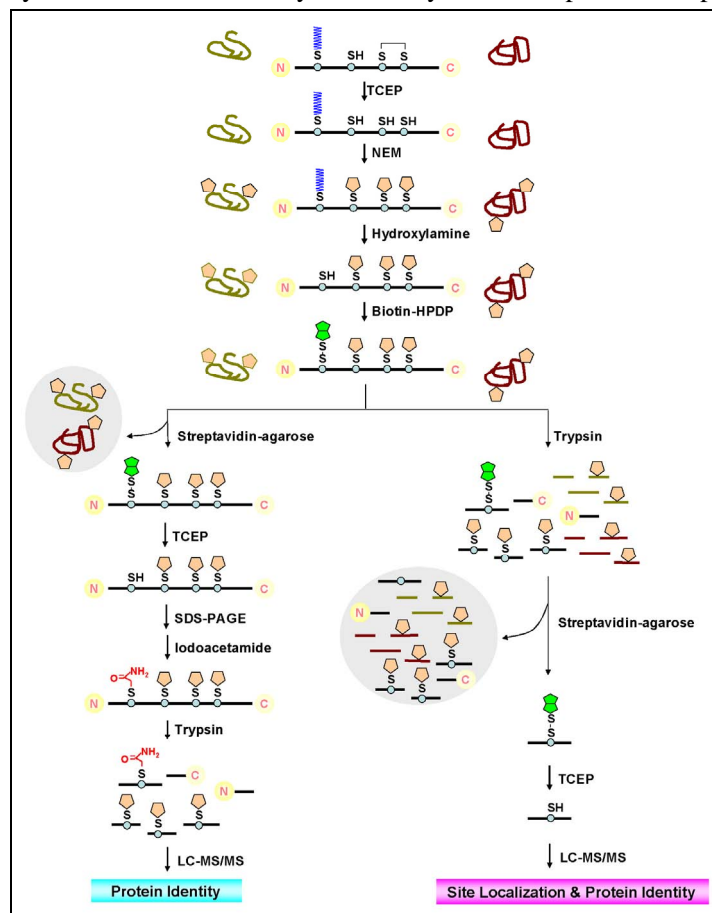


Figure 1. Schematic representation of the PalmPISC approach for large-scale palmitoyl protein enrichment and identification as well as palmitoylation site characterization. Upper: ABE reaction to replace palmitoyl groups with biotinyl groups. **Lower left:** protein-based procedure to enrich and identify palmitoyl proteins. **Lower right:** peptide-based procedure to enrich palmitoyl peptides and to localize palmitoylation sites.

2. Isolation of non-raft and raft-enriched membrane fractions

Lipid rafts isolated using conventional approaches are usually contaminated by nuclear fractions. To minimize this contamination, Dr. Rosalyn Adam modified a successive detergent extraction method originally developed by Solomon *et al.* (1,20) by pelleting nuclei prior to detergent extraction (21). Subsequently, I performed global analysis of proteins extracted from lipid raft-enriched fractions isolated from prostate cancer cells using the original as well as the modified procedures. This proteomic analysis validated that raft-enriched fractions isolated using the modified procedure are largely free of nuclear contamination (21). Using this modified procedure, I isolated raft-enriched and non-raft membrane fractions from the human prostate cancer cell line DU145 cells. Western blotting analysis validated that lipid raft markers caveolin-1 and Gi α_2 were greatly enriched in the raft-enriched fractions while non-raft marker β -tubulin was enriched in the non-raft fractions (Fig. 2). The results suggested that I obtained raft-enriched and non-raft membrane fractions as expected.

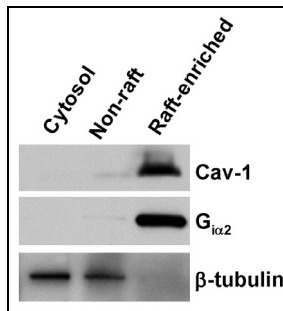


Figure 2. Isolation of lipid raft-enriched and non-raft membrane fractions. DU145 cell lysates were subjected to successive detergent extraction using a method that depletes nuclear proteins from the preparation (6). 10 µg proteins from cytoplasmic, non-raft, and lipid raft-enriched fractions were separated by SDS-PAGE, electrotransferred and immunoblotted with antibodies for the indicated proteins. The data are representative of three independent experiments.

3. Purification and separation of palmitoyl proteins

I used the PalmPISC method to purify palmitoyl proteins from raft-enriched and non-raft membranes isolated from DU145 cells. Figure 3 shows a representative gel image of experimental (EXP) and control (CON) groups of proteins, which were purified from equal amounts of total proteins extracted from non-raft (lane 2~3) and lipid raft-enriched (lane 4~5) membranes. Contaminating proteins were only co-purified at low levels (lane 3 vs. lane 2; lane 5 vs. lane 4). The SDS-PAGE protein patterns were different (lane 2 vs. lane 4), suggesting that some palmitoyl proteins are in fact concentrated in the raft-enriched fractions while others localize predominantly in the non-raft fractions. In addition, more proteins were found to be purified from the non-raft fractions than from the raft-enriched fractions (lane 2 vs. lane 4). This observation is *contrary to the general proposition that palmitoylation targets proteins to liquid-ordered lipid raft microdomains because of the saturated nature of palmitate*. There may be several reasons for this interesting finding. Firstly, tetraspanin-enriched microdomains, which can be disrupted by Triton X-100 at 4°C, contain a number of palmitoyl proteins (22). Secondly, some palmitoyl proteins (*e.g.*, Ras family proteins) are also prenylated, and prenylation may exclude modified proteins from lipid rafts (23). Indeed, only a few Ras-related proteins were identified in the present study in the lipid raft-enriched fractions (Table S1). Thirdly, a small fraction of palmitoyl proteins may also be S-acylated with other long-chain fatty acids (*e.g.*, C_{14:0} myristate, C_{16:1} palmitoleate, C_{18:0} stearate, C_{18:1} oleate, and C_{20:4} arachidonate) and unsaturated fatty acids may limit association with raft membranes. Finally, some palmitoylated transmembrane proteins have been found almost exclusively outside raft microdomains. For example, palmitoylation of tumor endothelial marker TEM8 excludes the protein from lipid rafts, while mutations of the cysteine residues target the protein to rafts (24).

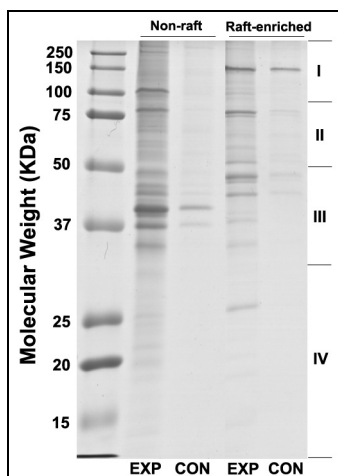


Figure 3. Electrophoretic analysis of +hydroxylamine (EXP) and –hydroxylamine (CON) samples purified from equal amounts of non-raft and lipid raft-enriched membrane fractions using PalmPISC. Purified proteins were resolved on a 12.5% SDS-PAGE gel and stained with Coomassie Brilliant Blue R-250 staining solution. Data represent at least three independent experiments.

4. Identification of putative palmitoyl proteins and peptides

Liquid chromatography-tandem mass spectrometry (LC-MS/MS) and spectral counting (19) analyses led to the identification of 66 known and 389 putative palmitoyl proteins as well as the localization of 23 known and 134 putative palmitoylation sites (Table S1~S7). Many well known palmitoyl proteins, such as caveolins, flotillins, Ras proteins, and G protein α subunits, were identified in this study. Moreover, among the 389 putative palmitoyl proteins, 97 can be metabolically labeled with a palmitate analogue, 17-octadecynoic acid (17-ODYA) (14) (Table S3). Figure 4 shows a representative MS/MS spectrum for protein identification, which was derived from the analysis of a doubly charged peptide (m/z 965.51) from erythrocyte band 7 integral membrane protein. Figure 5 shows a representative MS/MS spectrum for palmitoylation site localization, from which Cys17 was identified to be one potential palmitoylation site of flotillin-1 while Cys5 was not. In this study, all peptides were identified with high confidence ($p < 0.05$).

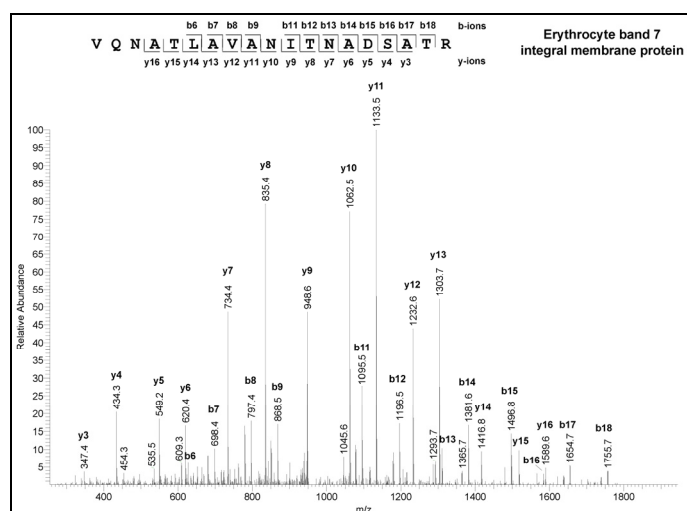


Figure 4. A representative tandem mass spectrum for LC-MS/MS analysis of palmitoyl proteins. MS/MS sequencing of a doubly charged peptide with m/z 965.51 led to the identification of the peptide VQNATLAVANITNADSATR, which is derived from erythrocyte band 7 integral membrane protein.

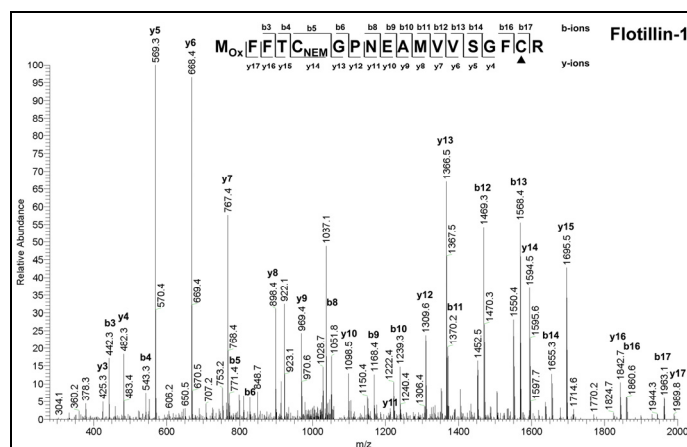


Figure 5. A representative tandem mass spectrum for palmitoylation site characterization. MS/MS analysis of a doubly charged peptide with m/z 1069.2 identified the peptide $M_{ox}FFTC_{NEM}GPNEAMVVSFGFCR$, derived from flotillin-1. The palmitoylation site Cys17 can be easily distinguished from nonpalmitoylated Cys5, which was previously blocked by NEM.

Notably, in this study, at least 7 palmitoyl acyltransferases (PATs) were identified to be putative palmitoyl proteins. DHHC5, 6, and 8 were found to be palmitoylated on three cysteine residues downstream of DHHC-CRD domain. Alignment analysis revealed that the three cysteine residues are embedded in a CCX₇₋₁₃CS/T motif (Fig. 6). The palmitoylation of the three cysteines results in the formation of a short loop, which may act as a scaffold to recruit specific substrates/regulators to the PATs and contribute to the their acyltransferase specificity and/or activity (Fig. 7).

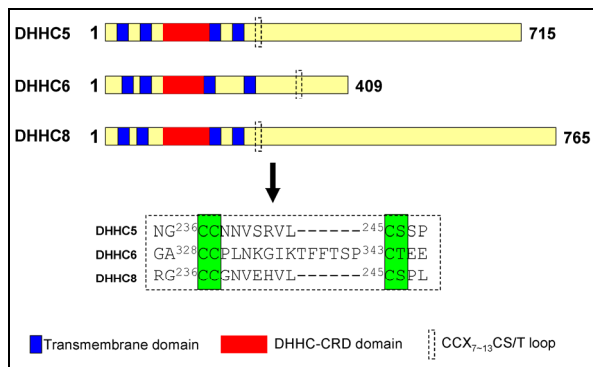


Figure 6. Illustration of primary structures of DHHC5, DHHC6, and DHHC8 proteins and alignment of CCX₇₋₁₃CS/T loops. Three putative palmitoylated cysteine residues are localized downstream of a conserved DHHC-CRD domain. The alignment analysis of the cysteines revealed a novel CCX₇₋₁₃CS/T motif.

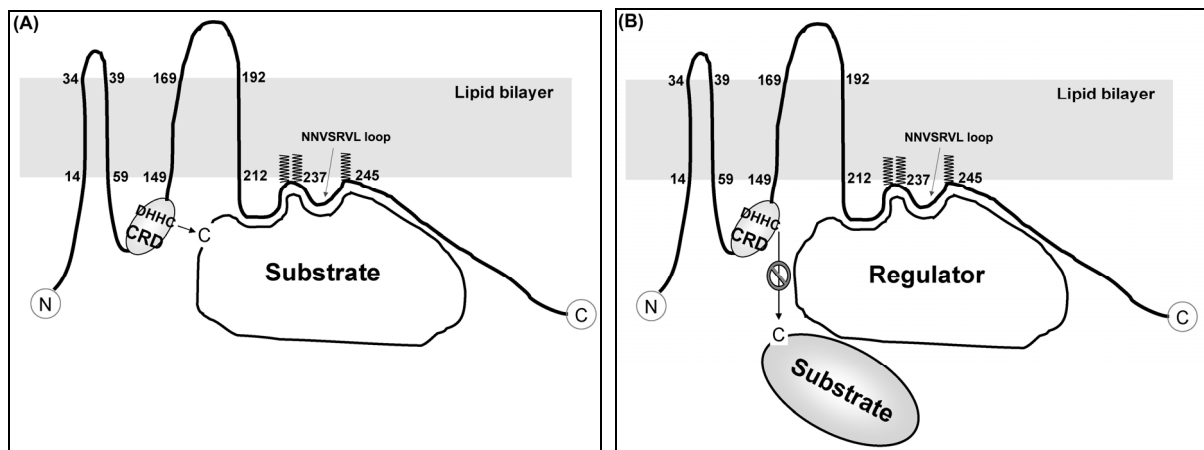


Figure 7. Two models for regulating PAT specificity and/or activity by protein palmitoylation. DHHC5 appears to be palmitoylated on three cysteine residues downstream of the DHHC-CRD domain. As a result, a seven amino acid (²³⁸NNVSRVL²⁴⁴) loop is formed, which may function as a scaffold to recruit specific substrates (A) or regulators (B) to DHHC5 and contribute to the specificity and/or activity of the PAT.

5. Validation of protein palmitoylation for ribosomal proteins RPL10A and RPL12 as well as acylprotein thioester 1 (APT1)

Ribosomal proteins are a major component of ribosomes and play key roles in cellular protein biosynthesis. They are generally localized in both the cytoplasm and nucleus but are also associated with rough endoplasmic reticulum (ER) membranes through the formation of complexes comprising ribosomes, nascent polypeptide chains, signal recognition particles (SRPs), and rough ER-associated SRP receptors. Surprisingly, the global analysis of palmitoyl proteins indicated that certain ribosomal subunits are targeted to lipid raft-enriched membranes through protein palmitoylation. To confirm this finding, immunoblotting and immunofluorescence analyses were performed. Localization of a pool of RPL10A and RPL12 proteins in lipid raft-enriched membranes was validated by Western blotting (Fig. 8A). ABE purification followed by Western blotting confirmed that both ribosomal proteins contain thioester bonds, suggesting that they are very likely palmitoylated (Fig. 8B). Very recently, an independent study showed that RPL10A and RPL12 can be metabolically labeled by a palmitate analogue, 17-ODYA (14), supporting our conclusion of the likely palmitoylation of the ribosomal proteins. Immunofluorescence analysis showed that a fraction of RPL10A proteins colocalize with CTxB, which has been widely exploited to visualize lipid rafts because it specifically binds to lipid raft-enriched GM1 ganglioside (Fig. 9, upper panels). 2-bromopalmitate (2-BP), a general protein palmitoylation inhibitor, treatment disrupted the localization of RPL10A in lipid rafts and resulted in the accumulation of the ribosomal protein in nuclei (probably nucleoli) (Fig. 9, lower panels).

Collectively, these data suggest that protein palmitoylation targets a fraction of certain ribosomal proteins to lipid rafts.

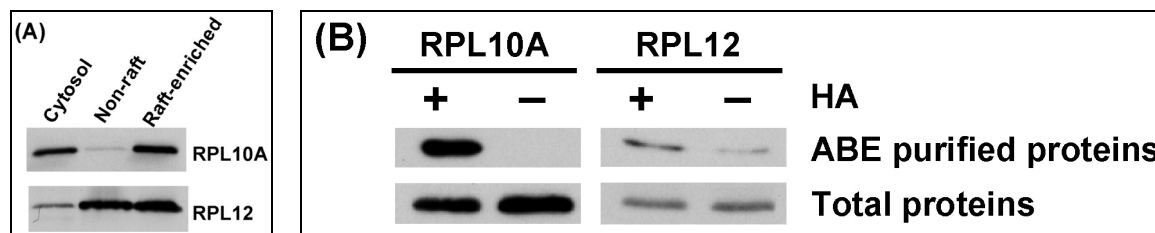


Figure 8. Ribosomal proteins RPL10A and RPL12 exist in lipid raft-enriched membranes and contain thioester bonds.

(A) 10 μ g proteins from the cytoplasmic, non-raft, and lipid raft-enriched fractions were separated by SDS-PAGE, electrotransferred, and immunoblotted with anti-RPL10A and anti-RPL12 antibodies. (B) Validation of the existence of thioester bonds in RPL10A and RPL12 proteins using ABE/immunoblotting. Proteins containing thioester bonds and controls were ABE purified from equal amounts of lipid raft-enriched fractions in the presence and absence of HA, respectively. RPL10A and RPL12 proteins were detected by Western blotting. As a control, portions of the unpurified samples, *i.e.*, total proteins, were also blotted. Data represent at least three independent experiments.

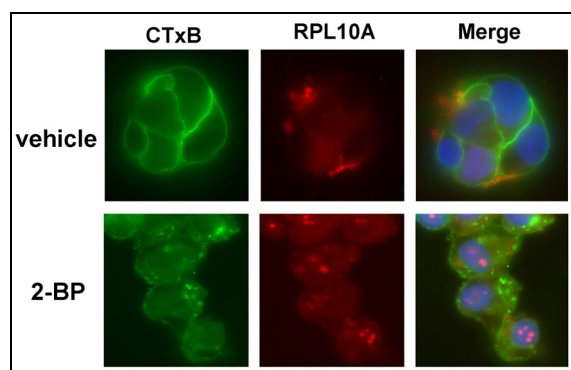


Figure 9. A pool of RPL10A proteins localizes in lipid rafts and the localization can be disrupted by the general palmitoylation inhibitor, 2-BP. DU145 cells treated with 100 μ M 2-BP (lower panels) or vehicle (0.1% ethanol, upper panels) were stained with 0.5 μ g/mL FITC-CTxB for 5 min, followed by staining with anti-RPL10A mAb (1:100) and Cy3-conjugated secondary antibody (1:250). Nuclei were counterstained with DAPI. Original magnification 63X.

APT1 is the only known cytoplasmic thioesterase. It depalmitoylates a number of proteins including Ras and G protein α subunits (25). This depalmitoylating enzyme primarily localizes in cytoplasm but can also be membrane-associated (26). However, little is known about the mechanism(s) that targets APT1 from cytosol to membranes. My global analysis of palmitoyl proteins indicated that APT1 may be tethered to membranes through protein palmitoylation. Western blotting analysis suggested that APT1 predominantly localizes in cytoplasm while a small and a tiny fractions of APT1 localizes in non-raft and raft-enriched membranes, respectively (Fig. 10A). ABE/immunoblotting analysis confirmed that APT1 contains thioester bonds (Fig. 10B). 2-BP treatment resulted in the inhibition of APT1 association with non-raft and raft-enriched membranes (Fig. 10C). Collectively, these data suggest that protein palmitoylation targets APT1 to membrane surfaces. The colocalization of APT1 with certain palmitoyl proteins, which are all membrane associated, may facilitates their depalmitoylation.

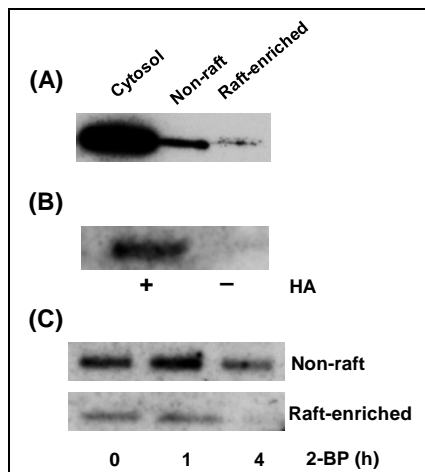


Figure 10. APT1 localizes in cytosol and non-raft and raft-enriched membranes with different abundance and its membrane association is regulated by protein palmitoylation. (A) 10 μ g proteins from the cytoplasmic, non-raft, and lipid raft-enriched fractions were separated by SDS-PAGE, electrotransferred, and immunoblotted with anti-APT1 antibody. (B) ABE/immunoblotting analysis suggested the existence of thioester bonds in APT1. Palmitoyl proteins were ABE purified from equal amounts of non-raft fractions in the presence and absence of HA, respectively. APT1 was detected by Western blotting. (C) The association of APT1 with non-raft and raft-enriched membranes can be inhibited by 2-BP, further validating that APT1 is a palmitoyl protein.

6. Bioinformatic analysis reveals two potential palmitoyl protein networks

Increasing evidence shows that reversible protein palmitoylation modulates protein-protein interactions and provides a mechanism for regulating the formation of multiprotein complexes. To investigate whether palmitoylated proteins interact with each other and form dynamic higher-order assemblies, I employed Ingenuity Pathway Analysis (IPA) software to analyze the potential for direct interactions among palmitoyl proteins identified with high confidence and currently known human palmitoyl proteins. This analysis revealed that 122 proteins form a large network via direct protein-protein interactions, in which two subnetworks emerged (Fig. 11). One subnetwork is centered round Cav-1, which directly interacts with 29 other palmitoyl proteins (Fig. 11A). The other subnetwork is based on several tetraspanins such as CD9, CD63, CD81, CD82, and CD151 (Fig. 11B). This analysis suggests that palmitoyl proteins are greatly enriched in the core complexes of caveolae and tetraspanin-enriched microdomains, both cholesterol-rich membrane structures.

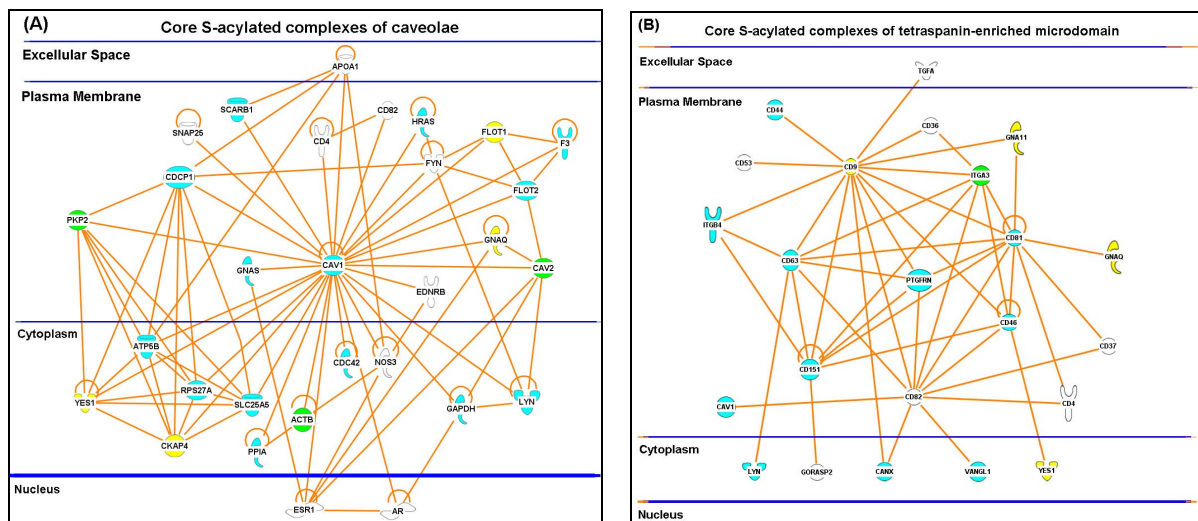


Figure 11. Virtual palmitoyl protein complexes. A number of palmitoyl proteins directly interact with each other and form a caveolin-1 complex (A) and a tetraspanin complex (B), suggesting that palmitoyl proteins are greatly enriched in the core complexes of caveolae and tetraspanin-enriched microdomains. Cyan, green, and yellow indicate highly probable palmitoyl proteins identified only by the protein-based procedure, only by the peptide-based procedure, and by both procedures, respectively. White indicates known human palmitoyl proteins that were not identified in DU145 cells.

7. Palmitoyl proteins play a key role in transmitting EGFR-Akt signals in DU145 cells

Very recently, our group published a paper in Cancer Research (27), in which we reported that EGF induced formation of secreted microvesicles from nonapoptotic membrane blebs in DU145 cells within a few minutes. Overexpression of lipid raft-resident myristoylated/palmitoylated Akt1 (MyrAkt1) also stimulated PCa cell blebbing, suggesting that EGF induces the formation of microvesicles through, at least in part, Akt1 present in lipid rafts. ***This is a novel function for lipid raft-resident Akt.*** I have performed comparative proteomics analysis on microvesicles isolated from LNCaP cells overexpressing MyrAkt1 or an irrelevant gene, LacZ. Multiple proteins of potential relevance to cancer progression such as pyruvate kinase M2 (PKM2) and programmed cell death 6 interacting protein (PDCD6IP) were identified in both types of LNCaP cells. Spectral counting (19) analysis showed that certain molecules were upregulated (*e.g.*, PKM2) or downregulated (*e.g.*, S100A7) in microvesicles shed from LNCaP/MyrAkt1 cells compared to those from LNCaP/LacZ cells. Immunoblotting analysis suggested that microvesicles shed from PCa cells contain numerous signaling proteins. We showed that these microvesicles are capable of activating phosphotyrosine and Akt pathway signaling as well as stimulating proliferation and migration in recipient cells. However, little is known about the molecular mechanisms underlying microvesicle formation in response to EGF stimulation or accumulation of Akt1 in lipid rafts. I have hypothesized that protein palmitoylation plays an active role in transmitting EGFR signaling based on the facts 1) that FASN, the key enzyme catalyzing the production of palmitate, is hyperactive in blebbing PCa cells, and 2) that protein palmitoylation, a reversible lipid modification, regulates the precise localization of signaling proteins in different microdomains.

To challenge this hypothesis, I treated DU145 cells with EGF for 0, 5, and 40 min after overnight serum starvation. I isolated non-raft and raft-enriched membranes using our modified successive detergent extraction method (21), purified palmitoyl proteins using the PalmPISC method, and resolved them into two SDS-gels in parallel. One gel was stained with highly sensitive Sypro Ruby stain and the gel images were shown in the upper panels of Figure 12. As can be seen, the palmitoyl protein patterns were not significantly changed by EGF stimulation. Proteins in the other gel were electrotransferred onto nitrocellular membrane and their tyrosine phosphorylation levels were detected by an anti-pTyr antibody. As shown in the middle and the lower panels of Figure 12, the tyrosine phosphorylation levels of total non-raft and raft proteins only slightly went up after EGF stimulation. This is probably because EGFR is constitutively active in DU145 cells due to its overexpression. Thus, DU145 cells have a high tyrosine phosphorylation baseline and the total tyrosine phosphorylation level is modestly changed in response to EGF treatment. In addition, because the very high molecular weight proteins are much harder to be electrotransferred than other proteins, only a small fraction of EGFR proteins were transferred onto nitrocellular membrane. Therefore, no strong tyrosine phosphorylation signals for EGFR were detected. However, interestingly, the tyrosine phosphorylation levels for certain palmitoyl proteins were remarkably regulated (Fig. 12, middle and lower panels).

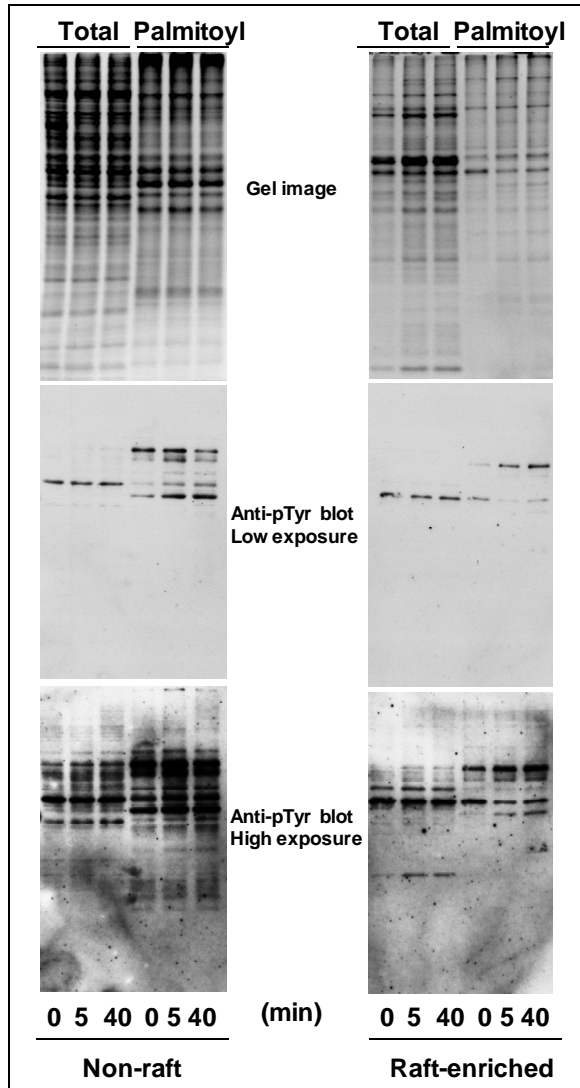


Figure 12. Tyrosine phosphorylation levels for certain palmitoyl proteins are remarkably changed in response to EGF stimulation of DU145 cells. **Upper:** Sypro Ruby stained gel images of total and purified palmitoyl proteins from non-raft (left) and raft-enriched (right) membranes, which were isolated from DU145 cells treated with 50 ng/mL EGF for 0, 5, and 40 min. As seen here, the pattern of palmitoyl proteins were almost unchanged, suggesting that abundant palmitoyl proteins were not significantly changed by EGF stimulation. **Middle and lower:** Tyrosine phosphorylation levels for total and palmitoyl proteins were detected by immunoblotting using anti-pTyr antibody (4G10). Notably, tyrosine phosphorylation levels for certain palmitoyl proteins were significantly regulated in response to EGF stimulation, while tyrosine phosphorylation levels for total non-raft or raft-enriched membrane proteins were only slightly upregulated.

I have proposed a model (Fig. 13) to interpret this interesting and unexpected finding. Tyrosine phosphorylation plays a major role in the formation of multiprotein signaling complexes and protein palmitoylation regulates the precise localization of proteins. Thus, the proteins being palmitoylated and tyrosine phosphorylated are likely to be essential for the formation of precisely localized signaling complexes. The remarkable regulation of tyrosine phosphorylated palmitoyl proteins indicates that certain precisely localized signaling complexes are significantly regulated in response to EGF stimulation of DU145 cells. Some of these precisely localized complexes may play a crucial role in the formation and secretion of microvesicles. This model also suggests that in addition to inhibiting certain tyrosine kinases, regulating the palmitoylation level of certain proteins by modulating the activity and/or specificity of certain PATs or APTs may also inhibit EGFR signaling. In other words, *the PATs or APTs involved in transmitting EGFR signaling may be excellent drug targets for advanced PCa.*

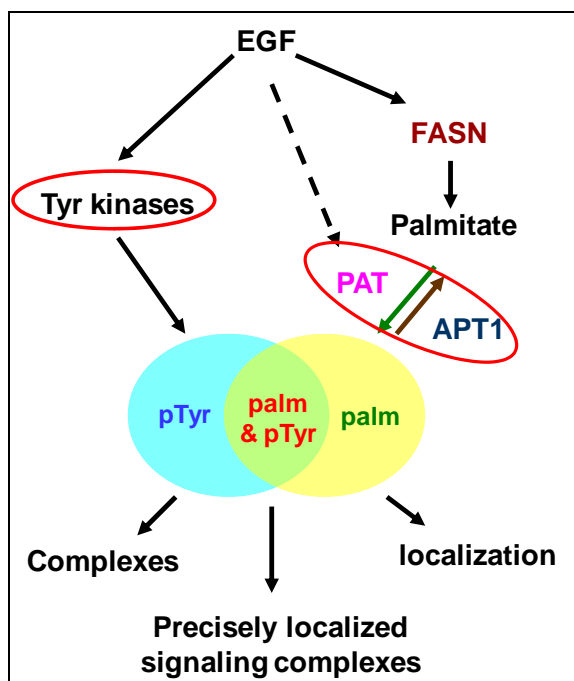


Figure 13. A model for the remarkable regulation of tyrosine phosphorylation levels for certain palmitoyl proteins in response to EGF treatment. EGF stimulation may activate tyrosine kinases, thus regulating the formation of multiprotein signaling complexes. EGF treatment also regulates protein palmitoylation, which determines the precise localization of modified proteins, through activating FASN and regulating the activities of certain PATs and/or APTs. The notable regulation of tyrosine phosphorylation levels for certain palmitoyl proteins indicates that some precisely localized signaling complexes are significantly regulated in response to EGF stimulation.

To identify the key palmitoyl proteins participating in transmitting EGFR signaling and quantitatively gauge their tyrosine phosphorylation level changes in response to EGF stimulation, we have started to employ SILAC, a state-of-the-art quantitative proteomics technology. The principle of triplex SILAC is straightforward. Three populations of cells are cultivated in a growth medium containing “light” (normal), “medium”, and “heavy” amino acids, respectively. Incorporation of the “medium” or “heavy” amino acids into a peptide leads to a known mass shift compared with the peptide that contains the light version of the amino acids (*e.g.*, 8 Da in the case of $^{13}\text{C}_6^{15}\text{N}_2$ -lysine), but no other chemical change. A trio of chemically identical peptides of different stable-isotope composition can be differentiated in a mass spectrometer owing to their mass difference. The ratio of peak intensities in the mass spectrum for such peptide trios accurately reflects the abundance ratio for the protein. As illustrated in Figure 14, DU145 cells will be cultured in “light”, “medium”, and “heavy” SILAC media and will be treated with EGF for 0, 5, and 40 min, respectively. Cells will be harvested and mixed at 1:1:1 ratio. Palmitoyl proteins/peptides will be purified using our PalmPISC method, followed by protein identification, palmitoylation site localization, and quantification. Tyrosine phosphorylated peptides will be purified from tryptic peptides derived from purified palmitoyl proteins or from total proteins extract from non-raft or raft-enriched membranes. These peptides will be identified and their tyrosine phosphorylation sites will be characterized. Moreover, tyrosine phosphorylation levels of these peptides will be quantitated. We believe this approach will lead in year 2 to the identification of key palmitoyl proteins involved in EGFR-Akt signaling.

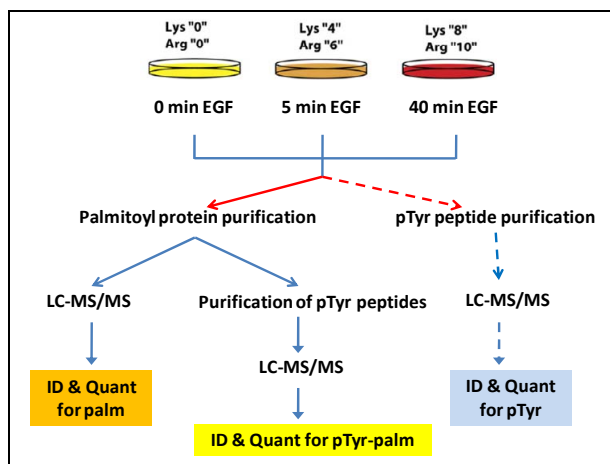


Figure 14. Workflow for the discovery of the key palmitoyl proteins involved in transmitting EGFR signaling in DU145 cells. Cells are cultured in SILAC media and stimulated with EGF for 0, 5, and 40 min. Palmitoyl proteins are purified using the PalmPISC method. Tyrosine phosphopeptides are enriched from palmitoyl proteins or total membrane proteins. Proteins/peptides will be identified and quantitated using LC-MS/MS and MaxQuant (www.maxquant.org), an open source program.

Key research Accomplishments

1. I have shown that many proteins are differentially expressed in microvesicles shed from LNCaP cells expressing MyrAkt1 and control cells expressing LacZ.
2. I have developed a novel method, PalmPISC, for the purification and identification of palmitoyl proteins and the characterization of palmitoylation sites.
3. I have shown that many palmitoyl proteins were also present in abundance outside the lipid raft compartment, although some palmitoyl proteins were indeed enriched in lipid rafts.
4. I have shown that three PATs, *i.e.*, DHHC5, 6, and 8, appear to be palmitoylated on three cysteines within a novel CCX₇₋₁₃CS/T motif downstream of a conserved DHHC-CRD domain, which may be a potential mechanism for regulating acyltransferase specificity and/or activity.
5. I have validated that ribosomal proteins RPL10A and RPL12 as well as thioesterase APT1 are tethered to lipid rafts and/or non-raft membranes through protein palmitoylation.
6. I have shown that palmitoyl proteins are greatly enriched in the core complexes of caveolae and tetraspanin-enriched microdomains.
7. I have shown that certain palmitoyl proteins, both within and outside of the lipid raft compartment, transmit EGFR-Akt signaling in DU145 cells.

Reportable Outcomes

Yang W., Di Vizio D., Kirchner M., Steen H., Freeman M.R. Proteome-scale characterization of human S-acylated proteins in lipid raft-enriched and non-raft membrane domains. *Molecular & Cellular Proteomics* (In revision)

Di Vizio, D., Kim, J., Hager, M. H., Morello, M., **Yang, W.**, Lafargue, C. J., True, L. D., Rubin, M. A., Adam, R. M., Beroukhim, R., Demichelis, F., Freeman, M. R. (2009) Oncosome formation in prostate cancer: Association with a region of frequent chromosomal deletion in metastatic disease. *Cancer Res* 69, 5601-5609

Conclusion

In summary, I have developed a novel method termed PalmPISC for the purification and identification of palmitoyl proteins and the localization of palmitoylation sites. Palmitoylproteomics analysis of lipid raft-enriched and non-raft membranes suggested that, although some palmitoyl proteins are in fact enriched in lipid raft compartment, many palmitoyl proteins are present in abundance *outside* lipid rafts. Three protein acyltransferases DHHC5, 6, and 8 appear to be palmitoylated on three cysteines within a novel CCX₇₋₁₃CS/T motif downstream of a conserved DHHC-CRD domain, which may be a potential mechanism for regulating acyltransferase specificity and/or activity. Immunoblotting and immunofluorescence analyses validated that ribosomal proteins RPL10A and RPL12 as well as thioesterase APT1 are tethered to membrane domains through protein palmitoylation. Bioinformatic analysis indicated that palmitoyl proteins are greatly enriched in the core complexes of caveolae and tetraspanin-enriched membranes. Functional palmitoylproteomics analysis suggested that certain palmitoyl proteins participate in transmitting EGFR signaling. The protein acyltransferases and acylprotein thioesterases regulating the palmitoylation levels of these key palmitoyl proteins may be novel targets for the inhibition of EGFR-Akt signaling, which can be exploited for the treatment of androgen-refractory prostate cancer.

References

1. Zhuang, L., Lin, J., Lu, M. L., Solomon, K. R., and Freeman, M. R. (2002) *Cancer Res* 62, 2227-2231
2. Zhuang, L., Kim, J., Adam, R. M., Solomon, K. R., and Freeman, M. R. (2005) *J Clin Invest* 115, 959-968
3. Adam, R. M., Mukhopadhyay, N. K., Kim, J., Di Vizio, D., Cinar, B., Boucher, K., Solomon, K. R., and Freeman, M. R. (2007) *Cancer Res* 67, 6238-6246
4. Cinar, B., Mukhopadhyay, N. K., Meng, G., and Freeman, M. R. (2007) *J Biol Chem* 282, 29584-29593
5. Cinar, B., Fang, P. K., Lutchman, M., Di Vizio, D., Adam, R. M., Pavlova, N., Rubin, M. A., Yelick, P. C., and Freeman, M. R. (2007) *EMBO J* 26, 4523-4534
6. Adam, R. M., Yang, W., Di Vizio, D., Mukhopadhyay, N. K., and Steen, H. (2008) *BMC Cell Biol* 9, 30
7. Simons, K., and Toomre, D. (2000) *Nat Rev Mol Cell Biol* 1, 31-39
8. Resh, M. D. (2006) *Sci STKE* 2006, re14
9. Swinnen, J. V., Heemers, H., van de Sande, T., de Schrijver, E., Brusselmans, K., Heyns, W., and Verhoeven, G. (2004) *J Steroid Biochem Mol Biol* 92, 273-279
10. Baron, A., Migita, T., Tang, D., and Loda, M. (2004) *J Cell Biochem* 91, 47-53
11. Menendez, J. A., and Lupu, R. (2007) *Nat Rev Cancer* 7, 763-777
12. Hang, H. C., Geutjes, E. J., Grotenbreg, G., Pollington, A. M., Bijlmakers, M. J., and Ploegh, H. L. (2007) *J Am Chem Soc* 129, 2744-2745
13. Kostiuk, M. A., Corvi, M. M., Keller, B. O., Plummer, G., Prescher, J. A., Hangauer, M. J., Bertozzi, C. R., Rajaiah, G., Falck, J. R., and Berthiaume, L. G. (2008) *FASEB J* 22, 721-732
14. Martin, B. R., and Cravatt, B. F. (2009) *Nat Methods* 6, 135-138
15. Drisdell, R. C., and Green, W. N. (2004) *Biotechniques* 36, 276-285
16. Roth, A. F., Wan, J., Bailey, A. O., Sun, B., Kuchar, J. A., Green, W. N., Phinney, B. S., Yates, J. R., 3rd, and Davis, N. G. (2006) *Cell* 125, 1003-1013
17. Kang, R., Wan, J., Arstikaitis, P., Takahashi, H., Huang, K., Bailey, A. O., Thompson, J. X., Roth, A. F., Drisdell, R. C., Mastro, R., Green, W. N., Yates, J. R., 3rd, Davis, N. G., and El-Husseini, A. (2008) *Nature* 456, 904-909

18. Zhang, J., Planey, S. L., Ceballos, C., Stevens, S. M., Jr., Keay, S. K., and Zacharias, D. A. (2008) *Mol Cell Proteomics* 7, 1378-1388
19. Liu, H., Sadygov, R. G., and Yates, J. R., 3rd. (2004) *Anal Chem* 76, 4193-4201
20. Solomon, K. R., Mallory, M. A., Hanify, K. A., and Finberg, R. W. (1998) *Biochem Biophys Res Commun* 242, 423-428
21. Adam, R. M., Yang, W., Di Vizio, D., Mukhopadhyay, N. K., and Steen, H. (2008) *BMC Cell Biol* 9, 30
22. Le Naour, F., Andre, M., Boucheix, C., and Rubinstein, E. (2006) *Proteomics* 6, 6447-6454
23. Melkonian, K. A., Ostermeyer, A. G., Chen, J. Z., Roth, M. G., and Brown, D. A. (1999) *J. Biol. Chem.* 274, 3910-3917
24. Abrami, L., Leppla, S. H., and van der Goot, F. G. (2006) *J Cell Biol* 172, 309-320
25. Zeidman, R., Jackson, C. S., and Magee, A. I. (2009) *Mol Membr Biol* 26, 32-41
26. Sim, D. S., Dilks, J. R., and Flaumenhaft, R. (2007) *Arterioscler Thromb Vasc Biol* 27, 1478-1485
27. Di Vizio, D., Kim, J., Hager, M. H., Morello, M., Yang, W., Lafargue, C. J., True, L. D., Rubin, M. A., Adam, R. M., Beroukhi, R., Demicheli, F., and Freeman, M. R. (2009) *Cancer Res* 69, 5601-5609

Appendices

Oncosome Formation in Prostate Cancer: Association with a Region of Frequent Chromosomal Deletion in Metastatic Disease

Dolores Di Vizio,^{1,2} Jayoung Kim,^{1,2} Martin H. Hager,^{1,2} Matteo Morello,^{1,2} Wei Yang,^{1,2} Christopher J. Lafargue,⁷ Lawrence D. True,⁶ Mark A. Rubin,⁷ Rosalyn M. Adam,^{1,2} Rameen Beroukhi,^{4,5,9} Francesca Demichelis,^{7,8} and Michael R. Freeman^{1,2,3}

¹The Urological Diseases Research Center, Children's Hospital Boston; Departments of ²Surgery and ³Biological Chemistry and Molecular Pharmacology, Harvard Medical School; ⁴Department of Medical Oncology and Cancer Biology, Dana-Farber Cancer Institute; and ⁵Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts; ⁶Department of Pathology, University of Washington Medical Center, Seattle, Washington; ⁷Department of Pathology and Laboratory Medicine and ⁸Institute for Computational Biomedicine, Weill Cornell Medical College, New York, New York; and ⁹Broad Institute of MIT and Harvard, Cambridge, Massachusetts

Abstract

Oncosomes have recently been described as membrane-derived microvesicles secreted by cancer cells, which transfer oncogenic signals and protein complexes across cell boundaries. Here, we show the rapid formation and secretion of oncosomes from DU145 and LNCaP human prostate cancer cells. Oncosome formation was stimulated by epidermal growth factor receptor activation and also by overexpression of membrane-targeted Akt1. Microvesicles shed from prostate cancer cells contained numerous signal transduction proteins and were capable of activating rapid phospho-tyrosine and Akt pathway signaling, and stimulating proliferation and migration, in recipient tumor cells. They also induced a stromal reaction in recipient normal cells. Knockdown of the actin nucleating protein Diaphanous Related Formin 3 (DRF3/Dia2) by RNA interference enhanced rates of oncosome formation, indicating that these structures resemble, and may be identical to, nonapoptotic membrane blebs, a feature of the amoeboid form of cell motility. Analysis of primary and metastatic human prostate tumors using 100K single nucleotide polymorphism arrays revealed a significantly higher frequency of deletion of the locus encoding DRF3 (*DIAPH3*) in metastatic tumors ($P = 0.001$) in comparison with organ-confined tumors. Fluorescence *in situ* hybridization confirmed increased chromosomal loss of *DIAPH3* in metastatic tumors in a different cohort of patients ($P = 0.006$). These data suggest that microvesicles shed from prostate cancer cells can alter the tumor microenvironment in a manner that may promote disease progression. They also show that DRF3 is a physiologically relevant protein that seems to regulate this process. [Cancer Res 2009;69(13):5601–9]

Introduction

Prostate cancer (PCa) is a major cause of cancer-related death in Western countries. Although the majority of cancers are unlikely to progress to end-stage disease, castration-resistant PCa is still a major clinical challenge. The development of effective therapies for advanced PCa requires an understanding of the processes that

promote the metastatic state. Cancer cells colonize distant sites using several strategies, including production of proteases that degrade extracellular matrix (1), and extension of lamellipodia, filopodia, and other dynamic cell processes that mediate migration (2). Formation of lamellipodia, which generate force at the front end of a migrating cell, requires actin filament assembly and the coordinated activity of multiple protein complexes that regulate assembly and disassembly of the cytoskeleton (3).

A less studied mode of cell motility, termed “amoeboid” movement, occurs as a result of nonapoptotic blebbing (4, 5). Plasma membrane blebs arise from actomyosin contractions near the cortical cytoskeleton, which create the opportunity for rapidly forming membrane protrusions to arise from hydrostatic pressure. Actin filament assembly is not required for the formation of nonapoptotic blebs, but force generated by actin filaments is required for bleb retraction. Bleb-associated movement is mediated by Rho-GTPase/ROCK signaling (6) and generates propulsive motion through a three-dimensional matrix in a manner that requires limited or no proteolysis (7). The mechanisms that control the amoeboid phenotype in tumor cells are poorly understood, as is the role of this process in malignant progression.

Oncosomes are recently discovered membranous microvesicles that have been implicated in rapid intercellular transfer of oncogenic information from glioblastoma to indolent glioma cells (8). Although this process resembles paracrine signaling, it involves intercellular transfer of a membrane-bound micro-organellar rather than a soluble protein such as a growth factor or cytokine. In the present study, we show that PCa cells shed membrane-bound vesicles in response to signal transducers. These structures are fairly large (0.5 to $\sim 5 \mu\text{m}$), originate from nonapoptotic blebs in response to signaling cues, and have biological activity in their free-floating state. We also identify the formin homology protein, DRF3/Dia2, as a protein that seems to functionally inhibit oncosome formation. We also provide the first evidence that chromosomal loss at the DRF3 locus (*DIAPH3*) is associated with metastatic PCa. Our results suggest the novel possibility that oncosomes may play a role in progression to metastatic disease through the controlled export of oncogenic protein complexes.

Materials and Methods

Reagents. Antibodies were from Biosource, Cell Signaling, BD Transduction, Santa Cruz Biotechnologies, Sigma, Covance, Inc., and Upstate. ZD1839 (gefitinib) was from AstraZeneca. FuGENE6 was from Roche. Other reagents were from Sigma. Anti-DRF3 monoclonal antibody was a gift from Dr. H. Higgs (Dartmouth Medical School, Hanover, NH).

Note: Supplementary data for this article are available at Cancer Research Online (<http://cancerres.aacrjournals.org/>).

Requests for reprints: Michael R. Freeman, Enders Research Laboratories, Rm 1161, Children's Hospital Boston, 300 Longwood Avenue, Boston, MA 02115. Phone: 617-919-2644; Fax: 617-730-0238; E-mail: michael.freeman@childrens.harvard.edu.

©2009 American Association for Cancer Research.

doi:10.1158/0008-5472.CAN-08-3860

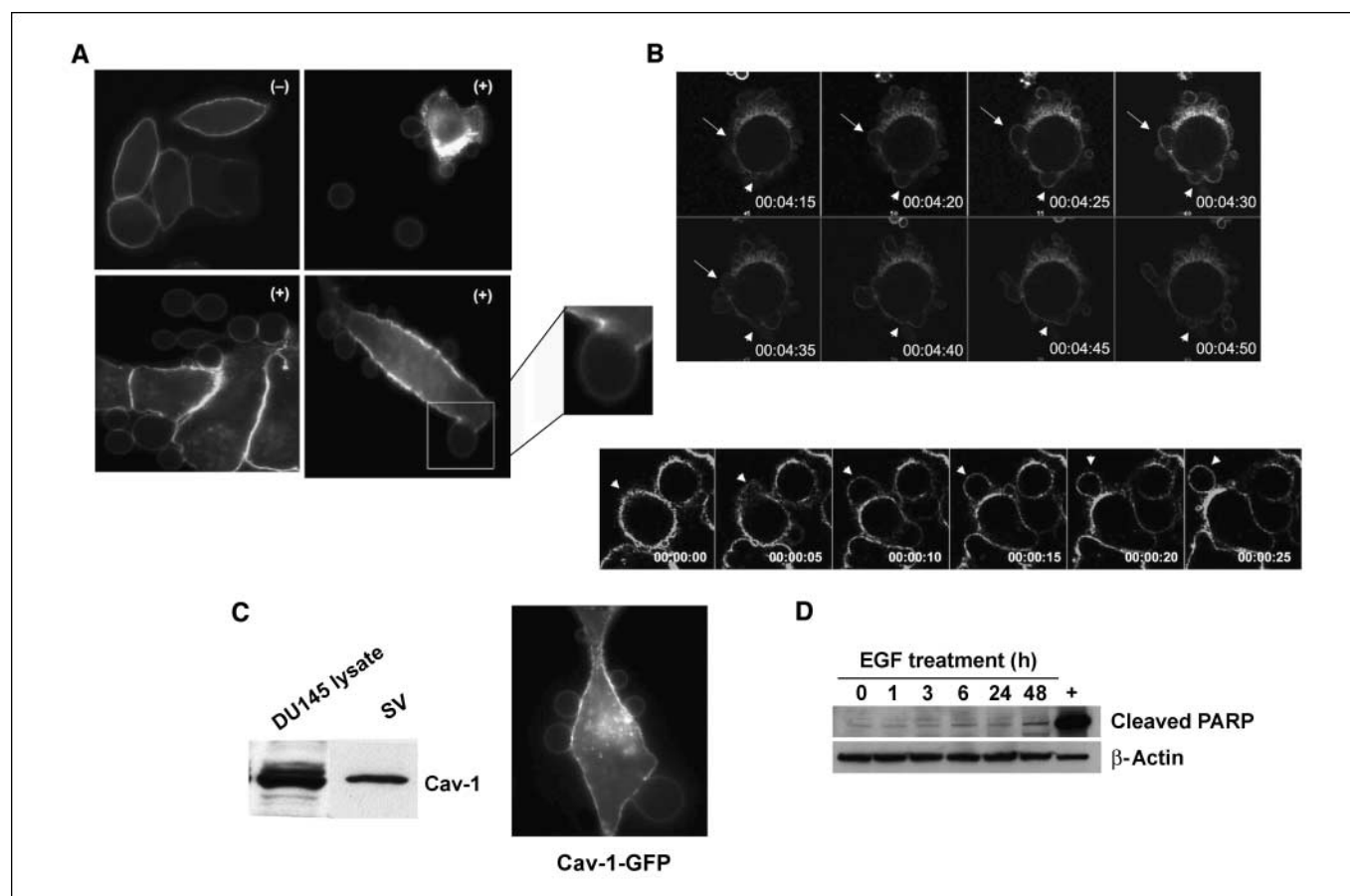


Figure 1. EGF induces formation of nonapoptotic membrane blebs. **A**, membrane staining with 0.5 $\mu\text{g/mL}$ FITC-CTxB for 5 min, after 3 h of treatment with: (–) vehicle or (+) EGF (50 ng/mL), and imaged by confocal microscopy ($\times 63$). All show DU145 cells, except at the top right, which shows a PC-3 cell and SV into the medium. *Inset*, a single, attached bleb at higher power. **B**, frames (5-s interval) from Movies 1 and 2 acquired by real-time confocal microscopy of DU145 cells expressing membrane-targeted pMEM-YFP, and treated with EGF. Two examples (*differently shaped arrows*) of bleb dynamics. **C**, lysates from whole cells and SV contain endogenous Cav-1, consistent with localization of a Cav-1-GFP fusion to membrane blebs. **D**, EGF does not induce apoptosis under these experimental conditions, as shown by an assay for cleaved PARP.

Cell culture and transfections. DU145, LNCaP, and WPMY-1 cell lines were from the American Type Culture Collection. hTERT-immortalized normal prostate epithelial cells (iPrEC), generously provided by Dr. W. Hahn (Dana-Farber Cancer Institute, Boston, MA) were kept in PrEGM medium. Stable transfectant cell populations (MyrAkt1, LacZ, HB-EGF, and Vo) were described (9, 10). Transient transfection [Cav-1-GFP (11) or pMEM-YFP (12)] were done using FuGENE6. These constructs were generously provided by Dr. M. Lisanti (Thomas Jefferson University, Philadelphia, PA) and Dr. D. Clapham (Harvard Medical School, Boston, MA), respectively.

Immunofluorescence microscopy. Cell membranes were labeled with FITC-conjugated cholera toxin B (CTxB) subunit (Sigma) or Alexa 594-conjugated CTxB (Molecular Probes) and analyzed as previously described (13).

Isolation of oncosomes and oncosome transfer assays. Shed microvesicles were collected from conditioned medium and purified essentially as described (8). Briefly, medium was subjected to two successive, rapid centrifugations at 300 and 12,000 g to eliminate cells and debris. Microvesicles were then pelleted by ultracentrifugation for 2 h at 100,000 g . Recovered material was resuspended in ice-cold PBS and quantified by measuring protein content. Recipient cells were serum-starved for 12 h and were subsequently treated with 20 μg of ultracentrifuged material.

Silencing of DRF3 expression. DU145 cells were transfected with ON-TARGETplus SMARTpool siRNA duplexes for the target sequence NM_030932, or with control nontargeting siRNA (Dharmacon, Inc.) using DharmaFECT1 reagent, for 72 h. Reverse transcription-PCR (RT-PCR) and

Western Blotting were used to validate specific silencing of DRF3 expression. *DIAPH3* gene-specific primer pair (5'-TATATAGGTACGCCAC CATGGAACGGCACCAGCCGCGC-3'/ 5'-AAGTTGGATATCCAGGCCATC-3') was used for the RT-PCR, and PCR products analyzed by agarose gel electrophoresis.

Mass spectrometry and label-free quantification. SDS-PAGE gel slices were subjected to in-gel digestion as described (14). Tryptic peptides were separated at circa 400 nL/min with 60 min linear gradients from 5% to 31% acetonitrile in 0.4% formic acid and analyzed using an LTQ ProteomeX ion trap mass spectrometer (Thermo Finnigan). Database searches were done as described (13) except that mass tolerance was set at ± 1.5 Da for MS/MS spectra. Proteins were identified with at least two unique peptides, with each peptide having an ion score no less than 40 ($P < 0.05$). Relative protein abundance was determined using label-free spectral counting (15).

Pathway enrichment and network analysis. The integrated software suite MetaCore (GeneGo) was used to map proteins into biological networks of human protein-protein, protein-DNA, and protein-compound interactions, metabolic and signaling pathways.¹⁰ For network analysis, two algorithms used were as follows: (a) the direct interaction algorithm to map direct protein-protein interaction; (b) the shortest path algorithm to map the shortest interaction pathway.

¹⁰ <http://www.genego.com>

Cell proliferation and migration assays. Cell proliferation was determined by viability assay (10). Cell migration was assessed using (a) *in vitro* wound healing assay and (b) cell migration chambers (Chemicon International, Inc.).

Single nucleotide polymorphism arrays. Human specimen collection and preparation have been described (16). Genomic DNA was hybridized to 100K SNP arrays (Affymetrix) according to the manufacturer's instructions. Arrays were scanned with a GeneChip Scanner 3000, and genotyping was done using Affymetrix Genotyping Tools Version 2.0. Probe-level signal intensities were normalized to a baseline array using invariant set normalization (17). Single nucleotide polymorphism (SNP)-level signal intensities were obtained using a model-based (PM/MM) method (17). Tumor data were normalized against data from normal tissue samples selected for similar baseline noise characteristics (18). Noise was further reduced using the segmentation algorithm Gain and Loss Analysis of DNA (19). Histogram analysis (18) was used to confirm that all tumors were sufficiently enriched to observe copy-number changes. Deletion at the *DIAPH3* locus was identified as segmented log₂ ratio of <−0.1, a value reached in only 0.5% of SNPs in data from normal tissue.

Dual color fluorescence *in situ* hybridization. *DIAPH3* gene alteration was assessed by fluorescence *in situ* hybridization (FISH) on tissue microarray sections with tissue samples from radical prostatectomy and a PCa progression tissue microarray (20). For the *DIAPH3* target probe, spanning the *DIAPH3* locus (chr13q21.2), the Biotin-14-dCTP-labeled BAC clones RP11-643G22 and RP11-638B12 (eventually conjugated to produce a red signal) were applied. For the reference probe, used to evaluate tumor cell ploidy on a stable area of chromosome 21, the Digoxigenin-11-dUTP-labeled BAC clone RP11-451M12 (eventually conjugated to produce a green signal) was applied. The BAC clones were from the BACPAC Resource Center, Children's Hospital Oakland Research Institute. Correct chromosomal probe localization was confirmed on normal lymphocytes metaphase preparations. Tissue hybridization, washing, and color detection were done as described (21). The samples were analyzed under a ×60 oil immersion objective using an Olympus BX-511 fluorescence microscope, a charge-coupled device camera,

and the CytoVision FISH software (Applied Imaging). Semiquantitative evaluation of the tests was done by D.D.V. and C.J.L. on at least 50 nuclei.

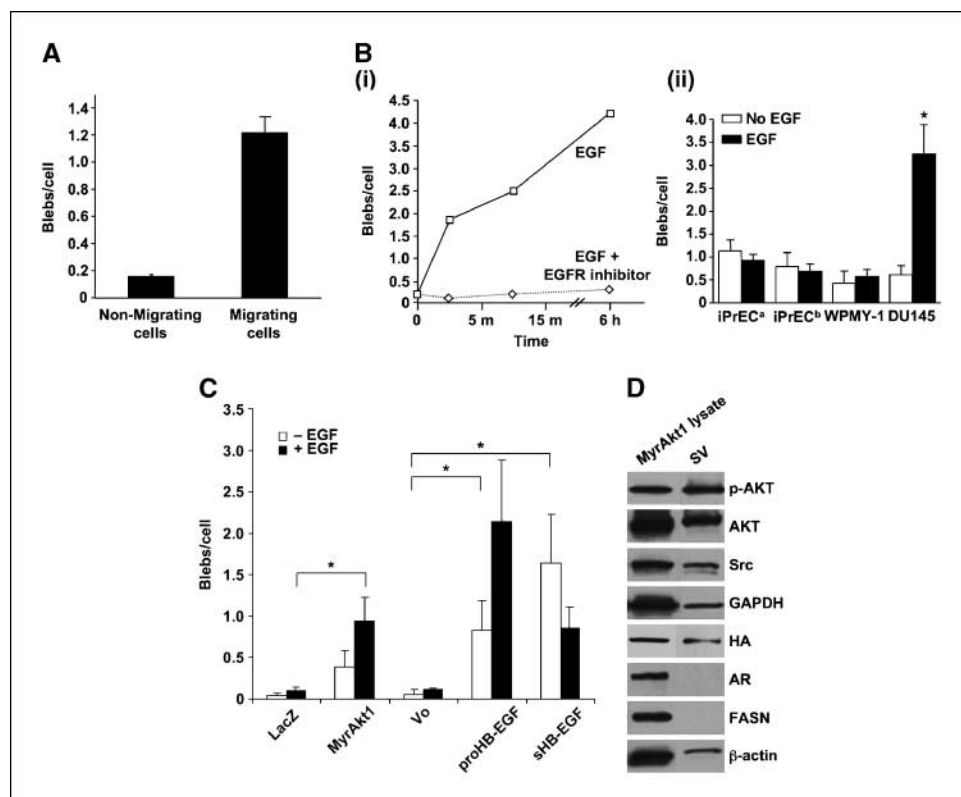
Real-time RT-PCR. Total RNA was isolated from WPMY-1 using TRIzol reagent, further purified using RNeasy columns and reverse-transcribed using iScript reagent (Bio-Rad Laboratories), according to the manufacturer's instructions. cDNAs were amplified with gene-specific primers for vimentin, or glyceraldehyde-3-phosphate dehydrogenase (GAPDH) using SYBR Green qPCR Master Mix. Human *PRKARIA* was used as an irrelevant gene. The relative abundance of a given transcript in control and treated cells was estimated by comparing the cycle threshold values for each sample following normalization to GAPDH.

Results

Inducible formation of nonapoptotic blebs in PCa cells. In experiments where DU145 human PCa cells were stimulated with epidermal growth factor (EGF), we noted extensive membrane blebbing (Fig. 1), which occurred immediately (~5 minutes) following growth factor treatment and persisted for 24 hours (Supplementary Fig. S1). Newly formed blebs were predominantly 0.5 to 5 μm in diameter and could be labeled with the ganglioside probe CTxB (Fig. 1A), a membrane-directed yellow fluorescent protein (pMEM-YFP; Fig. 1B; ref. 12) or the plasma membrane glycoprotein probe wheat germ agglutinin (data not shown). Sporadic bleb formation was also observed in vehicle-treated cells. Blebbing did not coincide with increased rates of cell death (Fig. 1D), indicating that these structures are nonapoptotic membrane blebs described in other cell types (22–26) but not to our knowledge in prostatic cells. Similar rapid blebbing was evoked from the PC-3 human PCa cell line in response to EGF (Fig. 1A).

Live confocal imaging of DU145 cells expressing pMEM-YFP and treated with EGF showed blebs emerging rapidly as protrusions,

Figure 2. Blebbing is associated with cell migration and activation of signaling, and results in production of SVs that contain membrane proteins. **A**, bleb formation in DU145 cells treated with EGF (50 ng/mL; 12 h) in a wound-healing assay. **B**, *i*, Bleb formation in DU145 cells treated with EGF or EGF plus gefitinib (ZD1839; 10 μmol/L). *ii*, bleb formation in prostate normal epithelial (iPrEC) and stromal (WPMY-1) cells, in comparison with DU145, with and without EGF. iPrEC^a were kept in PrEGM medium, which is serum free but contains EGF, whereas iPrEC^b were transferred to serum-free RPMI 12 h before treatment. **C**, bleb formation in LNCaP cells stably engineered to express MyrAkt1, pro-HB-EGF, or soluble (constitutively secreted) sHB-EGF. LacZ (irrelevant gene) and Vo (vector only) are negative controls. **D**, protein from whole cell lysates and SV from EGF-treated LNCaP/MyrAkt1 cells were blotted with the indicated antibodies.



which were sometimes retracted (Movie 1; Fig. 1B). Blebs were also completely extruded from the cell body and released into the medium (Movie 2; Fig. 1A and C). Isolation of shed vesicles (SV) by collection of media and ultracentrifugation indicated that they contained the membrane protein caveolin-1 (Cav-1; Fig. 1D), a PCa serum biomarker and an indicator of advanced disease (27). Consistent with this observation, blebs could also be decorated with Cav-1-GFP (Fig. 1D). An *in vitro* wound-healing assay showed that rates of bleb formation correlated with increased cell migration (Fig. 2A). The increase in rates of blebbing in response to EGF was completely suppressed by the EGFR inhibitor gefitinib (Fig. 2Bi).

We observed spontaneous blebbing in LNCaP PCa cells; however, basal rates of bleb formation were lower in LNCaP than in DU145, a more aggressive cell line. To determine whether blebbing would increase in response to activation of oncogenic signaling, we assessed the extent of bleb formation in LNCaP cells stably expressing the potent membrane-directed oncoprotein MyrAkt1 (9), the membrane-associated precursor form of the EGFR ligand HB-EGF (proHB-EGF), or a soluble form of HB-EGF (sHB-EGF) that is released constitutively into the medium (10). Blebbing was significantly increased in LNCaP cells expressing

either proHB-EGF or sHB-EGF in the absence of exogenous EGF (Fig. 2C). Addition of EGF further increased blebbing in MyrAkt1- and proHB-EGF-expressing cells (Fig. 2C). Consistent with their sustained export of high levels of sHB-EGF, EGF did not have a further stimulatory effect on LNCaP/sHB-EGF cells. Bleb formation in normal prostate epithelial and stromal cells was modest and unresponsive to EGF (Fig. 2Bi); however, in this case, blebbing was not a reflection of EGFR level or sensitivity to ligand (Supplementary Fig. S1B).

Bleb secretions contain numerous signal transduction proteins. Because secreted vesicles (SV) contained Cav-1, we hypothesized that they might contain other signaling proteins as cargo. SV from LNCaP/MyrAkt1 and LNCaP cells transfected with an irrelevant gene (LacZ) were isolated by collection of medium, followed by ultracentrifugation. SV contained the membrane-associated proteins Akt and Src (Fig. 2D); however, we did not detect the largely nuclear androgen receptor and the predominantly cytosolic enzyme fatty acid synthase, both of which are expressed at high levels in LNCaP cells. We detected HA-tagged MyrAkt1 in SV from LNCaP/MyrAkt1 cells (Fig. 2D); however, LNCaP/LacZ cells also produced SV that contained endogenous Akt1 (Supplementary Fig. S2A).

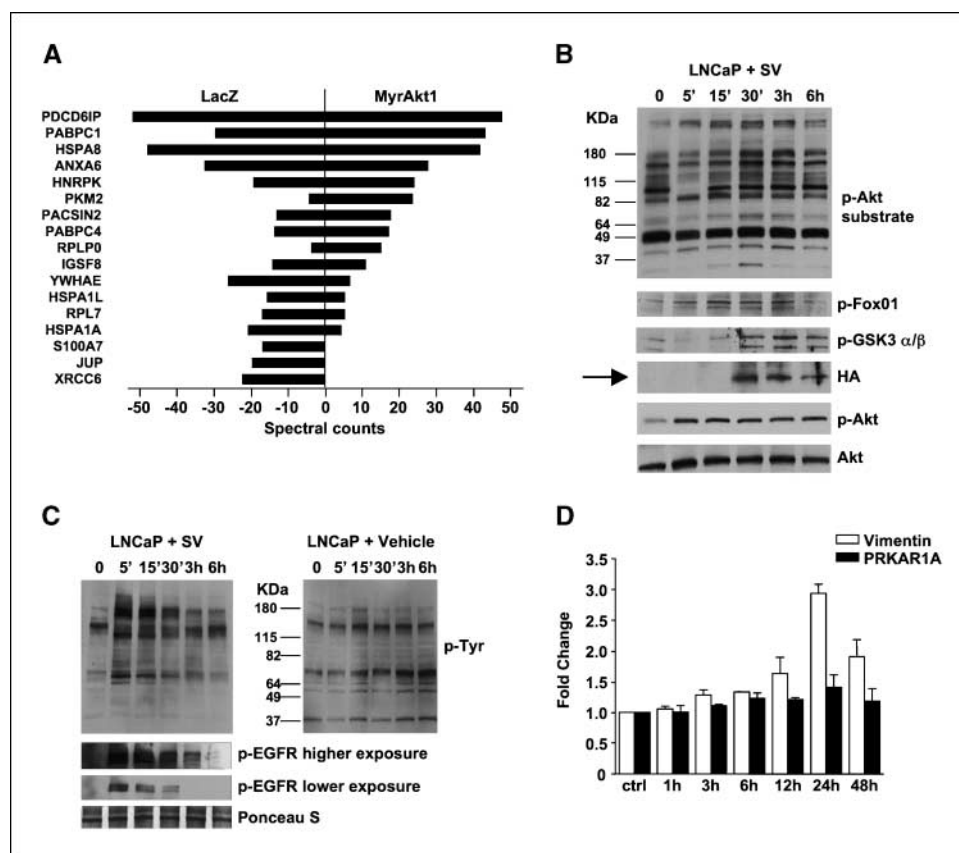


Figure 3. SVs exhibit oncosome activity. **A**, proteins identified by tandem mass spectrometry in bleb material and quantified using spectral counting. *PDCD6IP*, Programmed Cell Death 6 Interacting Protein; *PABPC1*, Poly(A) Binding Protein, Cytoplasmic 1; *HSPA8*, Heat Shock 70 kDa Protein 8; *ANXA6*, Annexin A 6; *hnRNP-K*, Heterogeneous Nuclear Ribonucleoprotein K; *PKM2*, Pyruvate Kinase M2; *PACIN2*, Protein Kinase C and Casein Kinase Substrate in Neurons 2; *PABPC4*, Poly(A) Binding Protein, Cytoplasmic 4; *RPLP0*, Ribosomal Protein Large P0-like Protein; *IGSF8*, Immunoglobulin Superfamily, member 8; *YWHAE*, Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, ϵ Polypeptide; *HSPA1L*, Heat Shock 70 kDa Protein 1-Like; *RPL7*, Ribosomal Protein L7; *HSPA1A*, Heat Shock 70 kDa protein 1A; *S100A7*, S100 calcium binding protein A7; *JUP*, Junction Plakoglobin; *XRCC6*, X-ray Repair Complementing defective repair in Chinese hamster cells 6. **B**, LNCaP/LacZ cells were exposed to SV obtained from EGF-treated LNCaP/MyrAkt1 cells. Blotting of whole cell lysates is shown. **C**, LNCaP/LacZ exposed to 20 μ g of SV or vehicle from EGF-treated LNCaP/MyrAkt1 cells and assessed for p-Tyr (top). Bottom, the results of blotting with p-EGFR antibody (p-Tyr¹⁰⁶⁸). **D**, WPMY-1 cells were exposed to LNCaP/MyrAkt1-derived SV for the indicated times. Vimentin mRNA was quantified by qRT-PCR in recipient cells, and normalized using GAPDH. An irrelevant gene, *PRKAR1A*, was used as control.

Table 1. Proteins identified by mass spectrometry were analyzed by MetaCore software (GeneGo, Inc.) using two algorithms in which the output is either an intracellular signaling pathway or a biological process

Pathway models	LacZ (-log P)	MyrAkt1(-logP)
Translation: elongation: termination	3.9	(N/s)
Cytoskeleton: regulation of cytoskeleton rearrangement	(N/s)	4.7
Cell cycle: meiosis	(N/s)	5.9
Cytoskeleton: cytoplasm microtubules	(N/s)	(N/s)
Inflammation: IL-6 signaling	(N/s)	4.1
DNA damage: check point	(N/s)	4.1
Inflammation: TREM1 signaling	(N/s)	3.9
Cell cycle: G1-S	(N/s)	3.6
Cell adhesion: cell junctions	(N/s)	3.6
Transduction: translation initiation	4.5	(N/s)
Biological process models	LacZ (-log P)	MyrAkt1(-logP)
Glycolysis and gluconeogenesis	(N/s)	(N/s)
Vitamin K metabolism	(N/s)	(N/s)
Transcription: role of heterochromatin protein(HPI) family in transcriptional silencing	(N/s)	1.5
Cell cycle: role of 14-3-3 proteins in cell cycle regulation	(N/s)	5.7
Translation: regulation of translation initiation	1.6	(N/s)
Cytoskeleton remodeling: neurofilament	(N/s)	(N/s)
Glycolysis and gluconeogenesis	(N/s)	(N/s)
Transcription: Role of AP in regulation of cellular metabolism	(N/s)	(N/s)
Cell cycle: spindle assembly and chromosome separation	(N/s)	(N/s)
Development: role of CDKS in neuronal development	(N/s)	(N/s)

NOTE: Significance was defined as *P* value of <0.05.

Abbreviation: N/s, not significant.

To identify protein cargo in SV in an unbiased manner, LNCaP/LacZ and LNCaP/MyrAkt1 SV protein was fractionated by SDS-PAGE. Two prominent zones containing the most abundant proteins ran at approximately 80 and 30 kDa (Supplementary Fig. S2B). These zones were excised and analyzed by tandem mass spectrometry. Each protein was identified from at least two unique peptides with an ion score of no less than 40 ($P < 0.01$). SV proteins were sorted according to their MOWSE scores and semiquantified using spectral counting (15). Numerous signaling proteins involved in cell metabolism, mRNA processing, and cell growth and motility were identified (Supplementary Table S1; Fig. 3A). The majority of SV proteins were present in both sublines, although as shown, there were some quantitative differences (only proteins with <15 spectral counts in at least one sample are shown). This result suggests the possibility of changes in SV protein composition with alterations in signal transduction (e.g., up-regulation Akt signaling in LNCaP/MyrAkt1 cells). Multiple proteins of potential relevance to cancer progression were found, including the following: (a) the cancer cell-specific isoform of pyruvate kinase M2 (PKM2), a phosphotyrosine-binding protein that promotes increased cell growth and tumor development (28); (b) programmed cell death 6 interacting protein (PDCD6IP), also known as Alix, recently shown to inhibit apoptosis (29); (c) poly(A)-binding protein 1 (PABPC1), which associates with paxillin and promotes cell migration; and (d) hnRNP-K, a multifunctional regulator of transcription and translation induced by extracellular growth promoting signals that enhance cancer cell proliferation (30).

Mass spectrometry data were analyzed using the MetaCore data mining tool¹⁰ to determine whether bleb/SV cargo could be organized into coherent networks and linked to one or more biological processes. Three statistically significant associations with GeneGo ontology pathway or biological process models, all related to mRNA translation, were identified using SV proteins from LNCaP/LacZ cells (Table 1). Interestingly, a much greater number of significant associations was detected using SV cargo from LNCaP/MyrAkt1 cells (nine such associations with LNCaP/Akt1 cells versus three seen with LNCaP/LacZ cells), including links to cytoskeletal rearrangement, cell cycle progression, inflammation, DNA damage, cell adhesion, and mRNA translation. These data suggest the possibility that the vesicles originating from plasma membrane blebs might be able to relay signals across cell boundaries in a manner similar to recently described glioblastoma-derived oncosomes (8).

Horizontal signaling. Because analysis of LNCaP SV cargo suggested that the bleb-derived material might possess bioactivities described for oncosomes, we asked whether LNCaP/MyrAkt1 SV are capable of altering signal transduction in recipient cells in a horizontal fashion. SV were isolated from LNCaP/MyrAkt1 cells and recovered material was quantified by determining protein content. Recipient LacZ cells exposed to SV from LNCaP/MyrAkt1 cells showed a time-dependent activation of the Akt pathway (Fig. 3B), as assessed using a consensus Akt-phosphorylated substrate antibody (31). Consistent with this, levels of active Akt1 (p-S473) and its phosphorylated targets GSK3 α/β (p-S21/9) and FoxO1 (p-S256) increased in a time-dependent manner. In these

experiments, HA-tagged MyrAkt1 was transferred to recipient cells (Fig. 3B, arrow). This finding shows that vesicles shed by LNCaP/MyrAkt1 cells possess activities associated with oncosomes. They also show that an oncoprotein (MyrAkt1) can be transferred across cell boundaries with SV as a vehicle. Consistent with these data, LNCaP/MyrAkt1 SV also evoked robust p-Tyr signaling and EGFR pathway activation in recipient cells (Fig. 3C). SV material also elicited increased levels of vimentin mRNA in WPMY-1 prostate stromal cells (Fig. 3D), suggesting that the vesicles are capable of evoking a stromal reaction (32).

The actin-nucleating protein DRF3/Dia2 inhibits bleb formation. Nonapoptotic membrane blebbing arises from membrane deformations resulting from actomyosin contraction (4) and has been linked to amoeboid cell motility and matrix invasion (23). These findings imply that actin remodeling may affect oncosome formation. To test this idea, we focused on Diaphanous-Related Formin 3 (DRF3), the human homologue of the mouse actin nucleating protein Drf3/mDia2 (33). DRF3 is encoded on chromosome 13q, which contains a region of genomic instability in PCa (34). An inhibitor of Drf3 was recently reported to induce

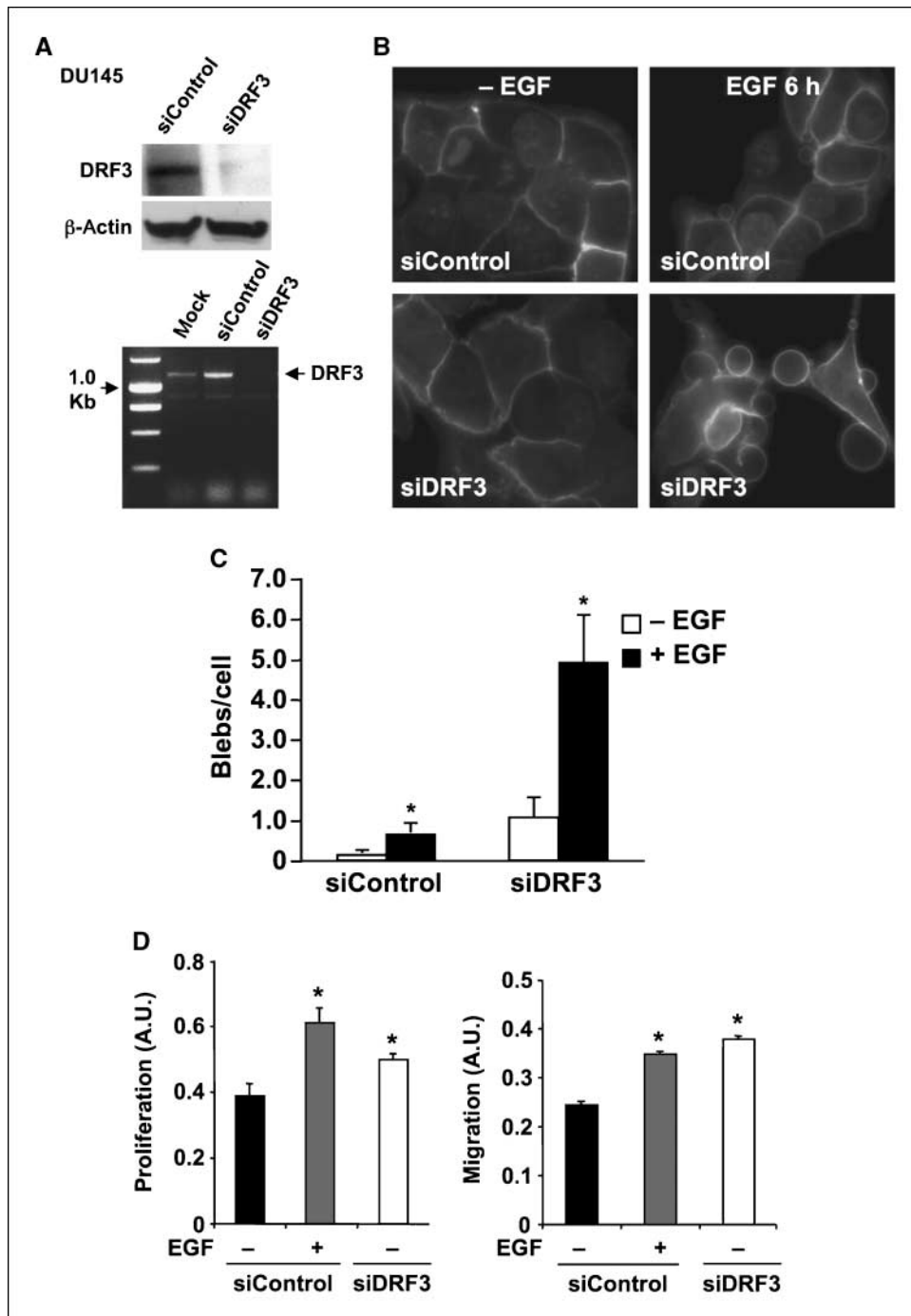


Figure 4. DRF3 knockdown by RNAi results in oncosome secretion. *A*, verification of *DIAPH3* gene silencing by siDRF3 in DU145 cells by Western blot (top) and RT-PCR (bottom). Control nontargeting siRNA was a negative control. *B*, FITC-CTxB staining of DU145 cells showing blebbing in siDRF3-transfected or siRNA control cells, with or without EGF (3 h; right). *C*, quantitative analysis of bleb formation in DU145 cells treated with siRNA for DRF3 or control siRNA, \pm EGF. *D*, proliferation assay (left) and migration assay (right) in DU145 cells treated with SV prepared from DU145 cells treated with siRNA control oligos, \pm EGF, or with DRF3-targeted oligos. *, $P < 0.05$.

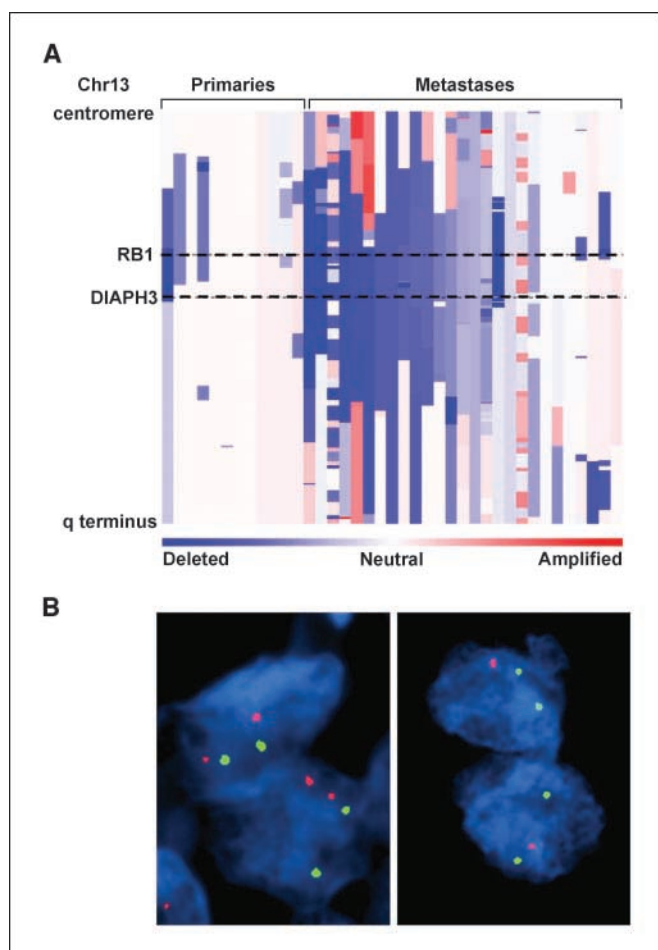


Figure 5. Genomic profiling of primary and metastatic PCa at the *DIAPH3* locus. **A**, amplifications (red) and deletions (blue), determined by segmentation analysis of normalized signal intensities from 100K SNP arrays (see Materials and Methods), are displayed for 39 PCas (X-axis; primaries and metastases are designated along the top) for the q arm of chromosome 13 (chromosomal positions indicated along the Y-axis include the centromere, q-terminus, and RB1 loci). **B**, *DIAPH3* fluorescent *in situ* hybridization was done by dual color FISH on PCa tissues. *Left*, FISH image shows both red signals (*DIAPH3* locus on chr13q21.2) and green signals (a stable region on chr21q22.12) in representative nuclei indicating no deletion of *DIAPH3* in tumor cells. *Right*, FISH image shows one red signal (*DIAPH3* locus on chr13q21.2) and two green signals (a stable region on chr21q22.12) in representative nuclei. Loss of the second red signal is consistent with deletion at *DIAPH3*. Original magnification of FISH images, $\times 60$ objective.

nonapoptotic blebbing (35), suggesting the possibility that DRF3 may oppose blebbing.

DRF3 knockdown by RNA interference (RNAi), using a pool of four siRNA oligos targeted to DRF3, dramatically increased bleb formation in the presence of EGF (Fig. 4A–C), a result that implicates cytoskeletal dynamics in the blebbing process. To determine whether SV derived from cells in which DRF3 had been knocked down would affect cell behavior in recipient cells, we did proliferation and migration assays using DU145 cells exposed to SV derived from DU145 cells in which DRF3 expression was reduced by RNAi. Cell proliferation and migration were increased in recipient cells exposed to SV isolated from DU145 cells treated with DRF3 siRNA, at a level quantitatively comparable with that elicited in donor cells by activation of EGFR alone (Fig. 4D).

Frequent chromosomal deletions at the *DIAPH3* locus in metastatic PCa. The above findings suggest that DRF3 is capable of inhibiting the blebbing/amoeboid phenotype. To determine the potential relevance of these observations to human PCa, we evaluated the human DRF3 locus (*DIAPH3*) for chromosomal alterations using 100K SNP arrays, profiling 12 primary PCa tumors and 27 metastatic tumors. A total of 19 (49%) of these tumors exhibited deletions at the *DIAPH3* locus (Fig. 5A), much higher than the overall 20% rate of deletion across the genome. Although all of these tumors, including the primaries, were sufficiently enriched to observe copy-number changes elsewhere in the genome, at the *DIAPH3* locus, deletions were observed more frequently among metastases [18 of 27 (67%)] than primaries [1 of 12 (8.3%); 2-sided Fisher's exact test, $P = 0.001$]. In a different cohort of patient samples, FISH, an alternative method, was used to assess the *DIAPH3* locus for chromosomal alterations. FISH results indicated chromosomal loss of *DIAPH3* in 7 of 35 (20%) primaries, and 9 of 14 (64%) metastases (Fig. 5B), confirming a significantly higher frequency of deletions in aggressive disease in comparison with primary tumors (2-sided Fisher's exact test, $P = 0.006$). *DIAPH3* deletion was not detected in benign tissues.

Discussion

In this study, we describe the production of nonapoptotic membrane blebs in human PCa cells in response to activation of oncogenic signaling (EGFR and Akt activation). Formation of these dynamic structures correlates with cell migration and, when shed from tumor cells, they elicit biological responses in recipient cells in a manner that resembles—but is mechanistically distinct from—paracrine signaling. We conclude that the microvesicles we have studied here are functionally equivalent to the bioactive oncosomes recently described as products of aggressive glioblastoma cells (8). We also identify the actin nucleating protein DRF3 as an endogenous inhibitor of oncosome formation. Analysis of primary and metastatic prostate tumors using high-density SNP arrays and FISH resulted in a highly significant association between chromosomal loss at the DRF3 (*DIAPH3*) locus and metastatic disease. To our knowledge, this is the first study that describes oncosome formation by PCa cells, the first to link formation of SV with nonapoptotic blebbing, and the first to provide evidence for involvement of the formin DRF3 in metastases in any tumor system. Oncosome activity was shown in two unrelated PCa cell line backgrounds, LNCaP and DU145, and similar membrane blebbing was evoked in PC-3 cells in response to EGF, suggesting that this is a general phenomenon. The precise relationship between the surprisingly large (0.5–5 μm) SV we have observed here by fluorescence microscopy, using several membrane probes, and the smaller (<0.1–1 μm) secreted vesicles reported by other groups (36, 37) remains to be determined.

The results of unbiased mass spectrometry studies, analysis of known proteins, and bioinformatics evaluation of SV cargo proteins are consistent with the finding that oncosome formation can result in transfer of membrane-associated protein complexes within the tumor microenvironment. Oncosomes might also be vectors of certain cancer progression markers that are detectable in the circulation. One such marker, Cav-1, identified in our study as oncosome cargo, is a circulating biomarker of metastatic PCa (13, 27, 38). Our data suggest that oncosome secretion is a mechanism whereby the integral membrane protein Cav-1 obtains access to the extracellular space, where it then becomes available

to act at distant sites. Another SV cargo protein identified by mass spectrometry is hnRNP-K, which we recently showed to be a novel Akt binding protein and regulator of androgen receptor translation (39). mRNA translation was repeatedly identified in the present study using the MetaCore software tool as a biological process that was significantly associated with bleb cargo proteins.

Our data indicate that the actin nucleator DRF3 is capable of inhibiting oncosome formation, because DRF3 knockdown by RNAi increased blebbing in DU145 cells, particularly in the presence of EGF. DRF3 is expressed by LNCaP, DU145, and PC-3 human prostate cell lines (data not shown). Formin homology proteins mediate cytoskeletal dynamics (9, 35) and, as a group, have been implicated in a wide range of cellular functions, including motility and vesicular trafficking (40, 41). The formin FHOD1, which exhibits 45% sequence homology to DRF3, was recently implicated in Src-dependent plasma membrane blebbing (42). Human DRF3 is not well-studied, although analyses of the mouse homologue Drf3, and the close mouse paralog, Drf1/mDia1, indicate that DRF3 likely mediates actin filament nucleation and elongation (43) and microtubule stability (44). A DRF3 interactor, the Diaphanous interacting protein DIP, was recently shown to promote plasma membrane blebbing by acting as a Dia inhibitor (35). Nonapoptotic membrane blebs can either dissociate from the cell or be retracted in an actin-dependent manner (4). Blebbing has been linked to the amoeboid form of cell movement (45) and our data indicate that DRF3 likely plays a role within a critical signaling node that controls the amoeboid phenotype. The finding that DRF3 silencing in SV donor cells resulted in increased cell proliferation and migration in SV recipient cells provides an important new link between: (a) blebbing and the amoeboid phenotype and (b) the production of vesicles that can propagate signals horizontally in the tumor microenvironment. These experimental data are consistent with our

analysis of human prostate tumors, indicating that chromosomal loss at the DRF3 coding region is associated with metastatic disease. Loss of function at the *DIAPH3* locus from somatic mutation may lead to alterations in the propensity toward invasion or metastasis. We are currently testing this hypothesis experimentally.

Our experiments suggest that oncosome transfer between tumor cells, or between tumor and stroma, could play a role in propagation of aggressive behavior within the tumor microenvironment. As pointed out by Al-Nedawi and colleagues (8), oncosome exchange is markedly different from paracrine effects induced by soluble ligands. However, this process could result in amplification of paracrine pathways through intercellular sharing of membrane-associated signaling complexes. Although our study focuses on PCa, a similar microvesicular transfer mechanism may operate in other tumor systems.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Acknowledgments

Received 10/3/08; revised 4/1/09; accepted 4/27/09; published OnlineFirst 6/23/09.

Grant support: National Institutes of Diabetes, Digestive and Kidney Diseases R3747556, P50 DK65298, National Cancer Institute (NCI) R01 CA112303 and DAMD17-03-2-0033 (M.R. Freeman), NCI K99 CA131472 (D. Di Vizio), DOD PCRP W81XWH-07-1-0148 (M.H. Hager), W81XWH-08-1-0139 (W. Yang), the AUA Foundation/GlaxoSmithKline (M.H. Hager), the Pacific Northwest Prostate Cancer Specialized Programs of Research Excellence CA97186, NCI P01CA085859 (L. True), K08CA122833 (R. Beroukhim), and R01CA116337-01A1 (M.A. Rubin and F. Demichelis). J. Kim is a Fishbein/ICA Scholar and a New York Academy of Medicine Edwin Beer Scholar.

The costs of publication of this article were defrayed in part by the payment of page charges. This article must therefore be hereby marked *advertisement* in accordance with 18 U.S.C. Section 1734 solely to indicate this fact.

We thank Dr. H. Steen for assistance with mass spectrometry and Paul Guthrie for technical assistance.

References

- Cao J, Chiarelli C, Richman O, Zarrabi K, Kozarekar P, Zucker S. Membrane type 1 matrix metalloproteinase induces epithelial-to-mesenchymal transition in prostate cancer. *J Biol Chem* 2008;283:6232-40.
- Wang HR, Zhang Y, Ozdamar B, et al. Regulation of cell polarity and protrusion formation by targeting RhoA for degradation. *Science* 2003;302:1775-9.
- Katoh H, Hiramoto K, Negishi M. Activation of Rac1 by RhoG regulates cell migration. *J Cell Sci* 2006;119:56-65.
- Paluch E, Sykes C, Prost J, Bornens M. Dynamic modes of the cortical actomyosin gel during cell locomotion and division. *Trends Cell Biol* 2006;16:5-10.
- Gadea G, Sanz-Moreno V, Self A, Godi A, Marshall CJ. DOCK10-mediated Cdc42 activation is necessary for amoeboid invasion of melanoma cells. *Curr Biol* 2008;18:1456-65.
- El-Sibai M, Pertz O, Pang H, et al. RhoA/ROCK-mediated switching between Cdc42- and Rac1-dependent protrusion in MTLn3 carcinoma cells. *Exp Cell Res* 2008;314:1540-52.
- Sahai E, Marshall CJ. Differing modes of tumour cell invasion have distinct requirements for Rho/ROCK signalling and extracellular proteolysis. *Nat Cell Biol* 2003;5:711-9.
- Al-Nedawi K, Meehan B, Micallef J, et al. Intercellular transfer of the oncogenic receptor EGFRvIII by microvesicles derived from tumour cells. *Nat Cell Biol* 2008;10:619-24.
- Adam RM, Mukhopadhyay NK, Kim J, et al. Cholesterol sensitivity of endogenous and myristoylated Akt. *Cancer Res* 2007;67:6238-46.
- Adam RM, Kim J, Lin J, et al. Heparin-binding epidermal growth factor-like growth factor stimulates androgen-independent prostate tumor growth and antagonizes androgen receptor function. *Endocrinology* 2002;143:4599-608.
- Volonte D, Galbiati F, Lisanti MP. Visualization of caveolin-1, a caveolar marker protein, in living cells using green fluorescent protein (GFP) chimeras. The subcellular distribution of caveolin-1 is modulated by cell-cell contact. *FEBS Lett* 1999;445:431-9.
- Oancea E, Wolfe JT, Clapham DE. Functional TRPM7 channels accumulate at the plasma membrane in response to fluid flow. *Circ Res* 2006;98:245-53.
- Adam RM, Yang W, Di Vizio D, Mukhopadhyay NK, Steen H. Rapid preparation of nuclei-depleted detergent-resistant membrane fractions suitable for proteomics analysis. *BMC Cell Biol* 2008;9:30.
- Yang W, Liu P, Liu Y, Wang Q, Tong Y, Ji J. Proteomic analysis of rat pheochromocytoma PC12 cells. *Proteomics* 2006;6:2982-90.
- Liu H, Sadygov RG, Yates JR, III. A model for random sampling and estimation of relative protein abundance in shotgun proteomics. *Anal Chem* 2004;76:4193-201.
- Hofer MD, Kuefer R, Huang W, et al. Prognostic factors in lymph node-positive prostate cancer. *Urology* 2006;67:1016-21.
- Li C, Wong WH. Model-based analysis of oligonucleotide arrays: expression index computation and outlier detection. *Proc Natl Acad Sci U S A* 2001;98:31-6.
- Beroukhim R, Getz G, Nghiemphu L, et al. Assessing the significance of chromosomal aberrations in cancer: methodology and application to glioma. *Proc Natl Acad Sci U S A* 2007;104:20007-12.
- Hu P, Stransky N, Thierry JP, Radvanyi F, Barillot E. Analysis of array CGH data: from signal ratio to gain and loss of DNA regions. *Bioinformatics* 2004;20:3413-22.
- Di Vizio D, Adam RM, Kim J, et al. Caveolin-1 interacts with a lipid raft-associated population of fatty acid synthase. *Cell Cycle* 2008;7:2257-67.
- Perner S, Mosquera JM, Demichelis F, et al. TMPRSS2-ERG fusion prostate cancer: an early molecular event associated with invasion. *Am J Surg Pathol* 2007;31:882-8.
- Fackler OT, Grosse R. Cell motility through plasma membrane blebbing. *J Cell Biol* 2008;181:879-84.
- Gadea G, de Toledo M, Anguille C, Roux P. Loss of p53 promotes RhoA-ROCK-dependent cell migration and invasion in 3D matrices. *J Cell Biol* 2007;178:23-30.
- Voura EB, Sandig M, Siu CH. Cell-cell interactions during transendothelial migration of tumor cells. *Microsc Res Tech* 1998;43:265-75.
- Charras GT, Hu CK, Coughlin M, Mitchison TJ. Reassembly of contractile actin cortex in cell blebs. *J Cell Biol* 2006;175:477-90.
- Tournaviti S, Hannemann S, Terjung S, et al. SH4-domain-induced plasma membrane dynamization promotes bleb-associated cell motility. *J Cell Sci* 2007;120:3820-9.
- Tahir SA, Yang G, Ebara S, et al. Secreted caveolin-1 stimulates cell survival/clonal growth and contributes to metastasis in androgen-insensitive prostate cancer. *Cancer Res* 2001;61:3882-5.
- Christofk HR, Vander Heiden MG, Harris MH, et al. The M2 splice isoform of pyruvate kinase is important for cancer metabolism and tumour growth. *Nature* 2008;452:230-3.
- Chatellard-Causse C, Blot B, Cristina N, Torch S, Missotten M, Sadoul R. Alix (ALG-2-interacting protein X), a protein involved in apoptosis, binds to endophilins and induces cytoplasmic vacuolization. *J Biol Chem* 2002;277:29108-15.

30. Mandal M, Vadlamudi R, Nguyen D, et al. Growth factors regulate heterogeneous nuclear ribonucleoprotein K expression and function. *J Biol Chem* 2001;276: 9699–704.
31. Zhang H, Zha X, Tan Y, et al. Phosphoprotein analysis using antibodies broadly reactive against phosphorylated motifs. *J Biol Chem* 2002;277:39379–87.
32. Mellick AS, Day CJ, Weinstein SR, Griffiths LR, Morrison NA. Differential gene expression in breast cancer cell lines and stroma-tumor differences in microdissected breast cancer biopsies revealed by display array analysis. *Int J Cancer* 2002;100:172–80.
33. Peng J, Wallar BJ, Flanders A, Swiatek PJ, Alberts AS. Disruption of the Diaphanous-related formin Drf1 gene encoding mDia1 reveals a role for Drf3 as an effector for Cdc42. *Curr Biol* 2003;13:534–45.
34. Dong JT, Boyd JC, Frierson HF, Jr. Loss of heterozygosity at 13q14 and 13q21 in high grade, high stage prostate cancer. *Prostate* 2001;49:166–71.
35. Eisenmann KM, Harris ES, Kitchen SM, Holman HA, Higgs HN, Alberts AS. Dia-interacting protein modulates formin-mediated actin assembly at the cell cortex. *Curr Biol* 2007;17:579–91.
36. Cocucci E, Racchetti G, Meldolesi J. Shedding microvesicles: artefacts no more. *Trends Cell Biol* 2009;19:43–51.
37. Jansen FH, Krijgsveld J, van Rijswijk A, et al. Exosomal secretion of cytoplasmic prostate cancer xenograft-derived proteins. *Mol Cell Proteomics*. Epub 2009 Feb 9.
38. Tahir SA, Yang G, Goltsov AA, et al. Tumor cell-secreted caveolin-1 has proangiogenic activities in prostate cancer. *Cancer Res* 2008;68:731–9.
39. Mukhopadhyay NK, Kim J, Cinar B, et al. Heterogeneous nuclear ribonucleoprotein K is a novel regulator of androgen receptor translation. *Cancer Res* 2009;69: 2210–8.
40. Schonichen A, Alexander M, Gasteier JE, Cuesta FE, Fackler OT, Geyer M. Biochemical characterization of the diaphanous autoregulatory interaction in the formin homology protein FHOD1. *J Biol Chem* 2006; 281:5084–93.
41. Rundle DR, Gorbysky G, Tsiokas L. PKD2 interacts and co-localizes with mDia1 to mitotic spindles of dividing cells: role of mDia1 IN PKD2 localization to mitotic spindles. *J Biol Chem* 2004;279:29728–39.
42. Hannemann S, Madrid R, Stastna J, et al. The diaphanous related formin FHOD1 associates with ROCK1 and promotes Src-dependent plasma membrane blebbing. *J Biol Chem* 2008;283:27891–903.
43. Kovar DR, Harris ES, Mahaffy R, Higgs HN, Pollard TD. Control of the assembly of ATP- and ADP-actin by formins and profilin. *Cell* 2006;124:423–35.
44. Jurdic P, Saltel F, Chabadel A, Destaing O. Podosome and sealing zone: specificity of the osteoclast model. *Eur J Cell Biol* 2006;85:195–202.
45. Yoshida K, Soldati T. Dissection of amoeboid movement into two mechanically distinct modes. *J Cell Sci* 2006;119:3833–44.

Supplemental Data

Proteome-scale Characterization of Human S-acylated Proteins in Lipid Raft-enriched and Non-raft Membrane Domains

Wei Yang, Dolores Di Vizio, Marc Kirchner, Hanno Steen, and Michael R. Freeman

Supplemental Tables include:

1. Table S1.
2. Table S2.
3. Table S3.
4. Table S4.
5. Table S5.
6. Table S6.
7. Table S7.

Table S1. Identification of human S-acylated proteins from non-raft and lipid raft-enriched fractions using the protein-based procedure.

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
1	+	IPI00739539	A26C1B	Ankrd26-like family C member 1B	Raft	7	90/1075	+	10.0	6.5	1.5	6	6	1.0	14	7	2.0
2	++	IPI00002230	AADACL1	Arylacetamide deacetylase-like 1	Non-raft	13	176/440	+	26.0	11.5	2.3	28	16	1.8	24	7	3.4
		IPI00002230	AADACL1	Arylacetamide deacetylase-like 1	Raft	3	41/440	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
3	–	IPI00027442	AARS	Alanyl-tRNA synthetase, cytoplasmic	Non-raft	5	67/968	–	1.0	2.0	0.5	2	3	0.7	0	1	0.0
4	+++++	IPI00065486	ABCB6	CDNA FLJ32464 fis, clone SKNMC1000251, highly similar to Homo sapiens MT-ABC transporter (MTABC) mRNA	Non-raft	9	139/766	+++++	7.0	0.0	23.3	11	0	36.7	3	0	10.0
5	++	IPI00008338	ABCC1	Isoform 2 of Multidrug resistance-associated protein 1	Non-raft	2	18/1472	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
6	+++++	IPI00006675	ABCC4	Multidrug resistance-associated protein 4	Non-raft	5	60/1325	+++++	3.5	0.0	11.7	4	0	13.3	3	0	10.0
7	–	IPI00303207	ABCE1	ATP-binding cassette sub-family E member 1	Non-raft	9	141/599	–	4.0	3.5	1.1	6	5	1.2	2	2	1.0
8	++	IPI00001539	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial	Non-raft	2	46/397	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
9	–	IPI00005040	ACADM	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	Non-raft	2	20/421	–	0.0	1.0	0.0	0	2	0.0	0	0	0.0
10	–	IPI00028031	ACADVL	Isoform 1 of Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	Non-raft	16	187/701	–	7.0	5.0	1.4	10	4	2.5	4	6	0.7
11	+++++	IPI00030363	ACAT1	Acetyl-CoA acetyltransferase, mitochondrial precursor	Non-raft	10	159/427	+++++	8.0	1.5	5.3	11	2	5.5	5	1	5.0
12	+++++	IPI00291419	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	Non-raft	8	135/397	+++++	6.5	0.5	13.0	10	1	10.0	3	0	10.0
13	–	IPI00021290	ACLY	ATP-citrate synthase	Non-raft	6	86/1101	–	1.5	2.5	0.6	3	4	0.8	0	1	0.0
14	+	IPI00017855	ACO2	Aconitate hydratase, mitochondrial precursor	Non-raft	6	78/780	+	2.5	1.0	2.5	3	2	1.5	2	0	6.7
15	++	IPI00003807	ACP2	Lysosomal acid phosphatase precursor	Non-raft	2	18/423	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
16	+	IPI00031397	ACSL3	Long-chain-fatty-acid--CoA ligase 3	Non-raft	10	143/720	+	5.0	2.0	2.5	6	2	3.0	4	2	2.0
17	++	IPI00029737	ACSL4	Isoform Long of Long-chain-fatty-acid--CoA ligase 4	Non-raft	5	75/711	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
18	–	IPI00021428	ACTA1	Actin, alpha skeletal muscle	Non-raft	13	123/377	–	19.0	21.0	0.9	17	21	0.8	21	21	1.0
		IPI00021428	ACTA1	Actin, alpha skeletal muscle	Raft	16	198/377	–	32.5	23.0	1.4	22	24	0.9	43	22	2.0
19	–	IPI00008603	ACTA2	Actin, aortic smooth muscle	Non-raft	5	78/377	–	2.0	1.5	1.3	4	3	1.3	0	0	0.0
20	–	IPI00021439	ACTB	Actin, cytoplasmic 1	Non-raft	25	252/375	–	47.5	47.5	1.0	61	54	1.1	34	41	0.8
		IPI00021439	ACTB	Actin, cytoplasmic 1	Raft	24	291/375	–	63.0	47.5	1.3	60	55	1.1	66	40	1.7
21	–	IPI00021440	ACTG1	Actin, cytoplasmic 2	Non-raft	25	252/375	–	48.5	47.5	1.0	60	57	1.1	37	38	1.0
		IPI00021440	ACTG1	Actin, cytoplasmic 2	Raft	25	277/375	–	64.5	48.5	1.3	66	57	1.2	63	40	1.6
22	+	IPI00013508	ACTN1	Alpha-actinin-1	Non-raft	14	182/892	+	7.0	4.5	1.6	9	4	2.3	5	5	1.0
		IPI00013508	ACTN1	Alpha-actinin-1	Raft	17	220/892	+	10.0	6.5	1.5	17	11	1.5	3	2	1.5
23	–	IPI00013808	ACTN4	Alpha-actinin-4	Non-raft	20	278/911	–	8.5	8.5	1.0	13	8	1.6	4	9	0.4
		IPI00013808	ACTN4	Alpha-actinin-4	Raft	32	402/911	–	13.5	12.5	1.1	27	25	1.1	0	0	0.0
24	–	IPI00028091	ACTR3	Actin-like protein 3	Non-raft	3	34/418	–	0.0	1.5	0.0	0	3	0.0	0	0	0.0
25	+++++	IPI00013897	ADAM10	ADAM 10 precursor	Non-raft	13	161/748	+++++	7.0	1.5	4.7	11	3	3.7	3	0	10.0
		IPI00013897	ADAM10	ADAM 10 precursor	Raft	2	24/748	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
26	+++	IPI00029606	ADAM17	Isoform B of ADAM 17 precursor	Non-raft	4	50/694	+++	2.0	0.0	6.7	1	0	3.3	3	0	10.0
		IPI00029606	ADAM17	Isoform B of ADAM 17 precursor	Raft	2	20/694	++	1.0	0.0	3.3	2	0	6.7	2	0	6.7
27	–	IPI00440932	ADAM9	Isoform 1 of ADAM 9 precursor	Non-raft	9	111/819	–	5.5	5.0	1.1	9	9	1.0	2	1	2.0
28	+++	IPI00025057	ADAR	Isoform 2 of Double-stranded RNA-specific adenosine deaminase	Raft	3	52/1200	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
29	++++	IPI00019141	AGPAT1	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	Non-raft	2	31/283	++++	2.5	0.0	8.3	2	0	6.7	3	0	10.0
30	+++	IPI00385128	AGPAT7	Isoform 1 of 1-acyl-sn-glycerol-3-phosphate acyltransferase eta	Non-raft	5	61/524	+++	3.0	0.5	6.0	4	1	4.0	2	0	6.7
31	–	IPI00010349	AGPS	Alkyldihydroxyacetonephosphate synthase, peroxisomal precursor	Non-raft	4	54/658	–	1.0	1.5	0.7	2	3	0.7	0	0	0.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
32	–	IPI00374563	AGRN	Agrin precursor	Non-raft	7	84/2045	–	0.5	3.5	0.1	1	7	0.1	0	0	0.0
		IPI00374563	AGRN	Agrin precursor	Raft	5	62/2045	+	2.0	1.0	2.0	4	2	2.0	0	0	0.0
33	–	IPI00012007	AHCY	Adenosylhomocysteinase	Non-raft	8	84/432	–	2.0	3.0	0.7	4	4	1.0	0	2	0.0
34	–	IPI00182938	AHCYL1	Putative adenosylhomocysteinase 2	Non-raft	2	26/530	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
35	–	IPI00021812	AHNAK	Neuroblast differentiation-associated protein AHNAK (Fragment)	Non-raft	4	56/5890	–	1.0	1.5	0.7	2	3	0.7	0	0	0.0
36	+++	IPI00856045	AHNAK2	Isoform 1 of protein AHNAK2	Non-raft	3	38/5795	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
37	++	IPI00000690	AIFM1	Isoform 1 of Programmed cell death protein 8, mitochondrial precursor	Non-raft	2	27/613	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
38	+	IPI00413641	AKR1B1	Aldose reductase	Non-raft	2	18/316	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
39	++	IPI00015102	ALCAM	CD166 antigen precursor	Non-raft	2	24/583	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
40	+++++	IPI00008982	ALDH18A1	Isoform Long of Delta 1-pyrroline-5-carboxylate synthetase	Non-raft	8	90/795	+++++	6.0	1.0	6.0	9	1	9.0	3	1	3.0
41	+++++	IPI00103467	ALDH1B1	Aldehyde dehydrogenase X, mitochondrial precursor	Non-raft	6	94/517	+++++	5.0	0.5	10.0	5	0	16.7	5	1	5.0
42	+	IPI00006663	ALDH2	Aldehyde dehydrogenase, mitochondrial precursor	Non-raft	4	58/517	+	2.5	1.0	2.5	2	2	1.0	3	0	10.0
43	+++++	IPI00018031	ALDH3B1	Isoform 1 of Aldehyde dehydrogenase 3B1	Non-raft	8	96/468	+++++	6.5	0.0	21.7	9	0	30.0	4	0	13.3
		IPI00018031	ALDH3B1	Isoform 1 of Aldehyde dehydrogenase 3B1	Raft	2	23/468	++++	2.5	0.0	8.3	3	0	10.0	2	0	6.7
44	+++	IPI00019888	ALDH5A1	Succinate semialdehyde dehydrogenase, mitochondrial precursor	Non-raft	2	28/535	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
45	+++	IPI00024990	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor	Non-raft	4	44/535	+++	2.0	0.0	6.7	1	0	3.3	3	0	10.0
46	–	IPI00221234	ALDH7A1	Similar to Aldehyde dehydrogenase family 7 member A1	Non-raft	4	55/539	–	1.5	1.5	1.0	2	3	0.7	1	0	3.3
47	–	IPI00465439	ALDOA	Fructose-bisphosphate aldolase A	Non-raft	21	251/364	–	18.5	16.5	1.1	26	24	1.1	11	9	1.2
48	–	IPI00022426	AMBP	AMBP protein precursor	Non-raft	3	31/352	–	0.0	2.0	0.0	0	0	0.0	0	4	0.0
		IPI00022426	AMBP	AMBP protein precursor	Raft	2	19/352	–	0.0	1.0	0.0	0	0	0.0	0	2	0.0
49	+++++	IPI00030431	ANTXR1	Isoform 1 of Anthrax toxin receptor 1 precursor	Non-raft	8	83/564	+++++	9.5	0.0	31.7	12	0	40.0	7	0	23.3
		IPI00030431	ANTXR1	Isoform 1 of Anthrax toxin receptor 1 precursor	Raft												

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
66	+++	IPI00013698	ASAH1	Acid ceramidase precursor	Non-raft	3	29/395	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
67	++	IPI00420014	ASCC3L1	U5 small nuclear ribonucleoprotein 200 kDa helicase	Raft	9	103/2136	++	3.5	1.0	3.5	7	2	3.5	0	0	0.0
68	+++	IPI00554777	ASNS	Asparagine synthetase	Non-raft	2	23/561	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
69	+	IPI00294834	ASPH	Aspartyl/asparaginyl beta-hydroxylase	Raft	3	43/758	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
		IPI00294834	ASPH	Aspartyl/asparaginyl beta-hydroxylase	Non-raft	8	93/758	+	4.0	1.5	2.7	6	3	2.0	2	0	6.7
70	+	IPI00550523	ATL3	hypothetical protein LOC25923	Non-raft	3	55/541	+	1.5	1.0	1.5	3	1	3.0	0	1	0.0
71	+++++	IPI00255653	ATP11A	Probable phospholipid-transporting ATPase 1H	Non-raft	8	103/1134	+++++	5.0	0.0	16.7	7	0	23.3	3	0	10.0
72	+++++	IPI00240793	ATP11B	Probable phospholipid-transporting ATPase 1F	Non-raft	6	97/1177	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
73	++++	IPI00177661	ATP13A3	PREDICTED: similar to Probable cation-transporting ATPase 13A3 (ATPase family homolog up-regulated in senescence cells 1) isoform 2	Non-raft	5	79/684	++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0
74	–	IPI00006482	ATP1A1	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	Non-raft	28	327/1023	–	20.0	15.0	1.3	27	20	1.4	13	10	1.3
		IPI00006482	ATP1A1	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	Raft	6	82/1023	–	2.5	2.0	1.3	5	4	1.3	0	0	0.0
75	+	IPI00219078	ATP2A2	Isoform SERCA2B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	Non-raft	28	345/1042	+	24.0	16.0	1.5	31	25	1.2	17	7	2.4
76	+	IPI00021695	ATP2B1	Isoform D of Plasma membrane calcium-transporting ATPase 1	Non-raft	7	79/1258	+	3.0	1.5	2.0	6	3	2.0	0	0	0.0
77	+	IPI00012490	ATP2B4	Isoform XD of Plasma membrane calcium-transporting ATPase 4	Non-raft	9	118/1241	+	4.5	1.5	3.0	9	3	3.0	0	0	0.0
78	++	IPI00220473	ATP2C1	Isoform 2 of Calcium-transporting ATPase type 2C member 1	Non-raft	2	28/888	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
79	+	IPI00440493	ATP5A1	ATP synthase subunit alpha, mitochondrial precursor	Non-raft	18	233/553	+	13.0	7.5	1.7	17	10	1.7	9	5	1.8
80	+++++	IPI00303476	ATP5B	ATP synthase subunit beta, mitochondrial precursor	Non-raft	5	76/529	+++++	4.5	1.0	4.5	5	2	2.5	4	0	13.3
81	++	IPI00219291	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 isoform 2b	Non-raft	2	24/88	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
82	++	IPI00007611	ATP5O	ATP synthase O subunit, mitochondrial precursor	Non-raft	2	12/213	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
83	++	IPI00024368	ATP9A	Isoform Long of Probable phospholipid-transporting ATPase 1IA	Non-raft	2	20/1047	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
84	–	IPI00180154	ATXN2	140 kDa protein	Raft	3	48/1313	–	0.0	1.5	0.0	0	3	0.0	0	0	0.0
85	++	IPI00456359	ATXN2L	Isoform 1 of Ataxin-2-like protein	Raft	2	34/1075	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
86	+++++	IPI00001891	AUP1	Isoform Long of Ancient ubiquitous protein 1 precursor	Non-raft	5	111/476	+++++	5.5	0.0	18.3	5	0	16.7	6	0	20.0
87	–	IPI00296992	AXL	AXL receptor tyrosine kinase isoform 1	Non-raft	3	41/894	–	1.5	2.0							

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
99	++++	IPI00006980	C14orf166	Protein C14orf166	Raft	10	129/244	++++	5.5	0.0	18.3	11	0	36.7	0	0	0.0
100	+++++	IPI00166051	C14orf24	Uncharacterized protein C14orf24	Non-raft	4	48/213	+++++	4.0	0.0	13.3	4	0	13.3	4	0	13.3
101	++	IPI00056357	C19orf10	Uncharacterized protein C19orf10 precursor	Non-raft	2	27/173	++	2.0	0.5	4.0	2	1	2.0	2	0	6.7
102	–	IPI00419849	C19orf2	RNA polymerase II subunit 5-mediating protein	Raft	3	34/535	–	1.0	1.0	1.0	2	2	1.0	0	0	0.0
103	+++++	IPI00303401	C1orf75	FLJ10874 protein	Non-raft	6	105/350	+++++	4.0	0.0	13.3	4	0	13.3	4	0	13.3
104	++	IPI00024913	C21orf33	Isoform Long of ES1 protein homolog, mitochondrial precursor	Non-raft	2	27/268	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
105	+	IPI00550689	C22orf28	UPF0027 protein C22orf28	Non-raft	3	38/505	+	1.5	0.5	3.0	1	1	1.0	2	0	6.7
		IPI00550689	C22orf28	UPF0027 protein C22orf28	Raft	6	70/505	+	3.0	1.0	3.0	5	1	5.0	1	1	1.0
106	++++	IPI00550440	C2orf18	Uncharacterized protein C2orf18 precursor	Non-raft	3	25/371	++++	4.5	0.0	15.0	7	0	23.3	2	0	6.7
		IPI00550440	C2orf18	Uncharacterized protein C2orf18 precursor	Raft	2	25/371	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
107	++++	IPI00024618	C3orf37	UPF0361 protein DC12	Raft	4	47/354	+++++	3.0	0.0	10.0	5	0	16.7	1	0	3.3
108	++	IPI00550571	C5orf15	Keratinocytes-associated transmembrane protein 2 precursor	Non-raft	2	21/265	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
109	+++	IPI00031617	C6orf125	Protein C6orf125	Non-raft	3	34/126	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
110	++	IPI00007067	C9orf19	Golgi-associated plant pathogenesis-related protein 1	Raft	2	26/154	++	1.0	0	3.3	2	0	6.7	0	0	0.0
111	++	IPI00012429	C9orf5	Isoform 2 of Protein C9orf5	Non-raft	2	26/886	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
112	+++	IPI00395627	CACYBP	Isoform 1 of Calyculin-binding protein	Non-raft	3	47/228	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
113	+++++	IPI00176427	CADM4	TSLC1-like 2	Non-raft	4	58/388	+++++	3.0	0.0	10.0	3	0	10.0	3	0	10.0
114	–	IPI00021536	CALML5	Calmodulin-like protein 5	Non-raft	3	48/146	–	0.5	1.5	0.3	1	0	3.3	0	3	0.0
115	–	IPI00020599	CALR	Calreticulin precursor	Non-raft	3	55/417	–	1.5	2.0	0.8	2	3	0.7	1	1	1.0
116	+++++	IPI00020984	CANX	Calnexin precursor	Non-raft	24	284/627	+++++	36.0	3.0	12.0	45	2	22.5	27	4	6.8
		IPI00020984	CANX	Calnexin precursor	Raft	5	66/627	+++++	4.0	0.5	8.0	4	0	13.3	4	1	4.0
117	+++	IPI00008274	CAP1	Adenylyl cyclase-associated protein 1	Non-raft	4	72/475	+++	2.0	0.0	6.7	3	0	10.0	1	0	3.3
118	++	IPI00643994	CAPN5	CDNA FLJ46245 fis, clone TESTI4020596, highly similar to Homo sapiens calpain 5	Non-raft	2	23/680	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
119	+	IPI00150961	CAPRIN1	membrane component chromosome 11 surface marker 1 isoform 1	Raft	10	152/709	+	9.5	5.5	1.7	15	7	2.1	4	4	1.0
120	–	IPI00026182	CAPZA2	F-actin capping protein alpha-2 subunit	Raft	3	42/286	–	1.0	1.0	1.0	1	1	1.0	1	1	1.0
121	+++	IPI00026185	CAPZB	Isoform 1 of F-actin capping protein subunit beta	Non-raft	4	53/303	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
		IPI00026185	CAPZB	Isoform 1 of F-actin capping protein subunit beta	Raft	5	63/303	+	2.5	1.0	2.5	4	2	2.0	1	0	3.3
122	++++	IPI00514301	CASK	Peripheral plasma membrane protein CASK	Non-raft	5	55/926	++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0
		IPI00514301	CASK	Peripheral plasma membrane protein CASK	Raft	3	30/926	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
123	–	IPI00013885	CASP14	Caspase-14 precursor	Non-raft	2	22/242	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
124	–	IPI00465436	CAT	Catalase	Non-raft	4	61/527	–	2.0	1.5	1.3	4	3	1.3	0	0	0.0
125	+++++	IPI00009236	CAV1	Caveolin 1	Non-raft	9	89/178	+++++	12.5	0.0	41.7	11	0	36.7	14	0	46.7
		IPI00009236	CAV1	Caveolin 1	Raft	11	130/178	+++++	11.0	0.0	36.7	13	0	43.3	9	0	30.0
126	++++	IPI00019870	CAV2	Isoform Alpha of Caveolin-2	Non-raft	2	42/162	+++	2.0	0.0	6.7	0	0	0.0	4	0	13.3
		IPI00019870	CAV2	Isoform Alpha of Caveolin-2	Raft	3	42/162	++++	3.0	0.0	10.0	2	0	6.7	4	0	13.3
127	++	IPI00410093	CCDC69	coiled-coil domain containing 69	Raft	2	23/296	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
128	++++	IPI00334743	CCNY	Isoform 2 of Cyclin fold protein 1	Non-raft	5	63/316	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
		IPI00334743	CCNY	Isoform 2 of Cyclin fold protein 1	Raft	3	43/316	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
129	++++	IPI00185371	CCNYL1	CDNA FLJ40432 fis, clone TESTI2039227	Non-raft	5	51/289	++++	3.0	0.0	10.0	5	0	16.7	1	0	3.3
130	–	IPI00297779	CCT2	T-complex protein 1 subunit beta	Non-raft	9	131/535	–	4.5	4.0	1.1	7	5	1.4	2	3	0.7
		IPI00297779	CCT2	T-complex protein 1 subunit beta	Raft	6	80/535	–	1.5	2.0	0.8	3	4	0.8	0	0	0.0
131	–	IPI00290770	CCT3	chaperonin containing TCP1, subunit 3 isoform b	Non-raft	5	60/544	–	2.5	2.5	1.0	4	3	1.3	1	2	0.5
132	–	IPI00302927	CCT4	T-complex protein 1 subunit delta	Non-raft	9	126/539	–	4.0	3.5	1.1	6	5	1.2	2	2	1.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
133	–	IPI00010720	CCT5	T-complex protein 1 subunit epsilon	Non-raft	6	69/541	–	3.0	3.5	0.9	3	4	0.8	3	3	1.0
		IPI00010720	CCT5	T-complex protein 1 subunit epsilon	Raft	5	63/541	–	1.5	2.0	0.8	3	4	0.8	0	0	0.0
134	–	IPI00027626	CCT6A	T-complex protein 1 subunit zeta	Non-raft	6	103/531	–	3.0	2.5	1.2	3	4	0.8	3	1	3.0
		IPI00027626	CCT6A	T-complex protein 1 subunit zeta	Raft	2	37/531	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
135	+	IPI00018465	CCT7	T-complex protein 1 subunit eta	Non-raft	6	101/543	+	3.5	1.5	2.3	6	3	2.0	1	0	3.3
136	–	IPI00302925	CCT8	Chaperonin containing TCP1, subunit 8	Non-raft	15	167/547	–	7.5	5.5	1.4	9	8	1.1	6	3	2.0
		IPI00302925	CCT8	Chaperonin containing TCP1, subunit 8	Raft	10	117/547	–	3.5	3.5	1.0	6	7	0.9	1	0	3.3
137	+++++	IPI00298851	CD151	CD151 antigen	Non-raft	3	32/253	+++++	6.5	0.0	21.7	7	0	23.3	6	0	20.0
138	++++	IPI00410488	CD276	Isoform 1 of CD276 antigen precursor	Non-raft	4	68/534	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
139	+++++	IPI00297160	CD44	CD44 antigen isoform 4 precursor	Non-raft	15	141/361	+++++	34.0	2.5	13.6	46	5	9.2	22	0	73.3
		IPI00297160	CD44	CD44 antigen isoform 4 precursor	Raft	14	125/361	+++++	34.5	0.5	69.0	55	0	183.3	14	1	14.0
140	+++++	IPI00219852	CD46	Isoform B of Membrane cofactor protein precursor	Non-raft	5	23/399	+++++	5.0	1.0	5.0	5	1	5.0	5	1	5.0
141	–	IPI00152418	CD55	Decay-accelerating factor splicing variant 4	Raft	2	18/525	–	1.0	1.0	1.0	1	1	1.0	1	1	1.0
142	+++	IPI00000059	CD58	LFA-3	Non-raft	2	12/162	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
143	+++++	IPI00215998	CD63	CD63 antigen	Non-raft	4	38/238	+++++	8.5	1.0	8.5	10	2	5.0	7	0	23.3
		IPI00215998	CD63	CD63 antigen	Raft	2	12/238	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
144	+++++	IPI00031713	CD70	Tumor necrosis factor ligand superfamily member 7	Non-raft	6	77/193	+++++	9.0	0.5	18.0	13	1	13.0	5	0	16.7
145	+++++	IPI00000190	CD81	CD81 antigen	Non-raft	3	27/236	+++++	10.0	0.0	33.3	10	0	33.3	10	0	33.3
		IPI00000190	CD81	CD81 antigen	Raft	2	23/236	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
146	+++++	IPI00215997	CD9	CD9 antigen	Non-raft	3	47/228	+++++	11.5	0.5	23.0	9	1	9.0	14	0	46.7
		IPI00215997	CD9	CD9 antigen	Raft	2	22/228	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
147	+	IPI00299412	CD97	Isoform 2 of CD97 antigen precursor	Non-raft	6	70/742	+	8.0	5.0	1.6	7	6	1.2	9	4	2.3
148	+++++	IPI00016786	CDC42	Isoform 2 of Cell division control protein 42 homolog precursor	Non-raft	5	79/191	+++++	5.0	1.5	3.3	5	1	5.0	5	2	2.5
149	++++	IPI00024973	CDC42SE2	CDC42 small effector 2	Non-raft	2	21/84	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
150	+++++	IPI00290039	CDCP1	Isoform 1 of CUB domain-containing protein 1 precursor	Non-raft	8	113/836	+++++	5.0	0.0	16.7	6	0	20.0	4	0	13.3
		IPI00290039	CDCP1	Isoform 1 of CUB domain-containing protein 1 precursor	Raft	5	77/836	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
151	–	IPI00000685	CDK7	Cell division protein kinase 7	Raft	2	24/346	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
152	+++	IPI00015713	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1	Non-raft	3	39/579	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
153	–	IPI00012011	CFL1	Cofilin-1	Non-raft	7	90/166	–	5.5	5.0	1.1	5	5	1.0	6	5	1.2
		IPI00012011	CFL1	Cofilin-1	Raft	6	82/166	+	4.5	2.5	1.8	6	3	2.0	3	2	1.5
154	+	IPI00413344	CFL2	Cofilin-2	Non-raft	5	68/166	+	3.0	1.5	2.0	3	2	1.5	3	1	3.0
		IPI00413344	CFL2	Cofilin-2	Raft	4	60/166	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
155	+++++	IPI00141318	CKAP4	Isoform 1 of Cytoskeleton-associated protein 4	Non-raft	26	324/602	+++++	24.5	0.5	49.0	29	1	29.0	20	0	66.7
		IPI00141318	CKAP4	Isoform 1 of Cytoskeleton-associated protein 4	Raft	23	300/602	+++++	24.5	0.0	81.7	28	0	93.3	21	0	70.0
156	–	IPI00022977	CKB	Creatine kinase B-type	Non-raft	5	62/381	–	2.0	2.0	1.0	3	3	1.0	1	1	1.0
157	++	IPI00045511	CLCC1	Mid-1-related chloride channel 1 isoform 1	Non-raft	2	22/551	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
158	++++	IPI00000691	CLDN1	Claudin-1	Non-raft	3	42/211	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
159	++++	IPI00059710	CLDN23	Claudin-23	Raft	5	80/292	++++	3.0	0.0	10.0	5	0	16.7	1	0	3.3
160	+++++	IPI00007364	CLDN3	Claudin-3	Non-raft	5	44/220	+++++	3.0	0.0	10.0	3	0	10.0	3	0	10.0
		IPI00007364	CLDN3	Claudin-3	Raft	2	15/220	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
161	++++	IPI00072743	CLDND1	Isoform 1 of Claudin domain-containing protein 1	Raft	5	62/253	++++	4.0	0.0	13.3	7	0	23.3	1	0	3.3
162	++	IPI00024776	CLGN	Calmegin precursor	Non-raft	2	20/610	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
163	+	IPI00010896	CLIC1	Chloride intracellular channel protein 1	Non-raft	6	87/241	+	3.0	1.5	2.0	5	1	5.0	1	2	0.5
164	++	IPI00001960	CLIC4	Chloride intracellular channel protein 4	Non-raft	2	21/253	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
165	–	IPI00024067	CLTC	clathrin heavy chain 1	Non-raft	28	394/1675	–	13.0	12.5	1.0	19	18	1.1	7	7	1.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
		IPI00024067	CLTC	clathrin heavy chain 1	Raft	14	175/1675	+	7.0	4.0	1.8	10	6	1.7	4	2	2.0
166	++	IPI00430813	CNBP	Isoform 2 of Cellular nucleic acid-binding protein	Non-raft	4	45/170	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
167	-	IPI00015262	CNN2	Calponin-2	Non-raft	2	35/309	-	0.0	1.0	0.0	0	2	0.0	0	0	0.0
168	-	IPI00166010	CNOT1	CCR4-NOT transcription complex, subunit 1 isoform a	Raft	6	64/2376	-	2.0	2.0	1.0	4	4	1.0	0	0	0.0
169	-	IPI00006552	CNOT7	CCR4-NOT transcription complex subunit 7	Raft	2	25/285	-	0.5	1.0	0.5	1	2	0.5	0	0	0.0
170	+++	IPI00220993	CNP	Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase	Non-raft	2	49/401	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
171	+++++	IPI00011284	COMT	Isoform Membrane-bound of Catechol O-methyltransferase	Non-raft	5	66/271	+++++	4.5	0.0	15.0	6	0	20.0	3	0	10.0
172	-	IPI00295857	COPA	Coatomer subunit alpha	Non-raft	13	167/1224	-	5.0	3.5	1.4	3	5	0.6	7	2	3.5
173	+	IPI00295851	COPB1	Coatomer subunit beta	Non-raft	4	62/953	+	2.5	1.5	1.7	4	2	2.0	1	1	1.0
174	-	IPI00220219	COPB2	Coatomer subunit beta'	Non-raft	6	64/906	-	2.0	3.0	0.7	3	5	0.6	1	1	1.0
175	-	IPI00001890	COPG	98 kDa protein	Non-raft	3	38/874	-	0.0	2.0	0.0	0	0	0.0	0	4	0.0
176	++	IPI00007058	CORO1B	Coronin-1B	Non-raft	4	65/489	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
177	-	IPI00008453	CORO1C	Coronin-1C	Non-raft	7	99/527	-	3.5	2.5	1.4	6	2	3.0	2	2	1.0
		IPI00008453	CORO1C	Coronin-1C	Raft	20	254/527	-	12.5	12.0	1.0	18	17	1.1	7	7	1.0
178	+	IPI00017510	COX2	Cytochrome c oxidase subunit 2	Non-raft	4	53/227	+	1.5	1.0	1.5	0	1	0.0	3	1	3.0
179	++++	IPI00027078	CPD	Carboxypeptidase D precursor	Non-raft	5	52/1380	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
180	-	IPI00026270	CPM	Carboxypeptidase M precursor	Raft	2	18/443	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
181	++	IPI00032038	CPT1A	Isoform 1 of Carnitine O-palmitoyltransferase I, liver isoform	Non-raft	3	39/773	++	2.0	0.5	4.0	3	1	3.0	1	0	3.3
182	-	IPI00016457	CRAT	Isoform 1 of Carnitine O-acetyltransferase	Non-raft	2	26/626	-	0.5	0.5	1.0	0	1	0.0	1	0	3.3
183	-	IPI00025366	CS	Citrate synthase, mitochondrial precursor	Non-raft	2	27/466	-	0.0	1.0	0.0	0	1	0.0	0	1	0.0
184	+++	IPI00219823	CSNK1G1	Isoform 1S of Casein kinase I isoform gamma-1	Raft	4	58/393	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
185	+++	IPI00297767	CSNK1G2	Casein kinase I isoform gamma-2	Non-raft	2	30/415	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
		IPI00297767	CSNK1G2	Casein kinase I isoform gamma-2	Raft	4	52/415	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
186	+++++	IPI00181294	CSNK1G3	Isoform 1 of Casein kinase I isoform gamma-3	Raft	9	139/447	+++++	6.0	0.0	20.0	9	0	30.0	3	0	10.0
187	+	IPI00442073	CSRP1	Cysteine and glycine-rich protein 1	Non-raft	2	25/193	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
188	+++++	IPI00009633	CTDSP1	Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1	Non-raft	5	55/261	+++++	4.0	0.0	13.3	4	0	13.3	4	0	13.3
		IPI00009633	CTDSP1	Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1	Raft	4	46/261	++++	2.5	0.0	8.3	4	0	13.3	2	0	6.7
189	+++	IPI00024826	CTDSPL	CTD small phosphatase-like protein	Non-raft	2	21/340	+++	1.5	0.0	5.0	0	0	0.0	3	0	10.0
190	++	IPI00215948	CTNNA1	Isoform 1 of Catenin alpha-1	Non-raft	7	105/906	+	2.5	1.0	2.5	5	2	2.5	0	0	0.0
		IPI00215948	CTNNA1	Isoform 1 of Catenin alpha-1	Raft	5	81/906	+++	2.5	0.5	5.0	5	1	5.0	0	0	0.0
191	+	IPI00017292	CTNNB1	Isoform 1 of Catenin beta-1	Non-raft	6	65/781	+	3.0	1.0	3.0	6	2	3.0	0	0	0.0
192	+++++	IPI00182469	CTNND1	Isoform 1AB of Catenin delta-1	Non-raft	28	388/963	+++++	29.5	1.0	29.5	35	1	35.0	24	1	24.0
		IPI00182469	CTNND1	Isoform 1AB of Catenin delta-1	Raft	9	152/963	++++	4.5	0.0	15.0	8	0	26.7	1	0	3.3
193	+++++	IPI00019146	CXADR	Isoform 1 of Coxsackievirus and adenovirus receptor precursor	Non-raft	14	207/365	+++++	19.5	0.0	65.0	23	0	76.7	16	0	53.3
		IPI00019146	CXADR	Isoform 1 of Coxsackievirus and adenovirus receptor precursor	Raft	2	25/365	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
194	++	IPI00019994	CXorf15	Gamma-taxilin	Raft	2	20/528	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
195	++++	IPI00303954	CYB5B	cytochrome b5 outer mitochondrial membrane precursor	Non-raft	4	70/150	++++	2.5	0.0	8.3	3	0	10.0	2	0	6.7
196	++	IPI00102928	CYB5D2	Cytochrome b5 domain containing 2	Non-raft	2	27/264	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
197	-	IPI00029264	CYC1	Cytochrome c1, heme protein, mitochondrial precursor	Non-raft	2	28/325	-	1.0	1.0	1.0	1	1	1.0	1	1	1.0
198	+	IPI00644231	CYFIP1	cytoplasmic FMR1 interacting protein 1 isoform a	Non-raft	4	46/1253	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
199	++++	IPI00337800	DAAM1	Isoform 1 of Disheveled-associated activator of morphogenesis 1	Non-raft	5	62/1078	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
200	+++++	IPI00385987	DAGLB	Isoform 1 of Sn1-specific diacylglycerol lipase beta	Non-raft	7	91/717	+++++	5.5	0.0	18.3	6	0	20.0	5	0	16.7
201	-	IPI00216951	DARS	Aspartyl-tRNA synthetase, cytoplasmic	Non-raft	7	97/501	-	2.5	2.5	1.0	4	4	1.0	1	1	1.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
202	++	IPI00003406	DBN1	Drebrin	Raft	10	119/649	++	5.0	1.5	3.3	9	3	3.0	1	0	3.3
203	–	IPI00027547	DCD	Dermcidin precursor	Non-raft	2	14/110	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
		IPI00027547	DCD	Dermcidin precursor	Raft	2	28/110	–	1.0	3.5	0.3	2	7	0.3	0	0	0.0
204	++	IPI00300567	DCI	Isoform 1 of 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	Non-raft	4	41/302	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
205	+++++	IPI00217282	DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3	Non-raft	4	64/304	+++++	3.5	0.0	11.7	4	0	13.3	3	0	10.0
		IPI00217282	DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3	Raft	9	127/304	+++++	6.5	0.0	21.7	7	0	23.3	6	0	20.0
206	+	IPI00297084	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase precursor	Non-raft	11	149/456	+	9.0	5.0	1.8	11	9	1.2	7	1	7.0
		IPI00297084	DDOST	dolichyl-diphosphooligosaccharide-protein glycosyltransferase precursor	Raft	5	75/456	+	2.0	1.0	2.0	2	2	1.0	2	0	6.7
207	–	IPI00293655	DDX1	ATP-dependent RNA helicase DDX1	Raft	4	69/740	–	2.0	2.0	1.0	4	4	1.0	0	0	0.0
208	–	IPI00023785	DDX17	Isoform 1 of Probable ATP-dependent RNA helicase DDX17	Non-raft	8	96/729	+	4.0	2.5	1.6	6	4	1.5	2	1	2.0
		IPI00023785	DDX17	Isoform 1 of Probable ATP-dependent RNA helicase DDX17	Raft	10	122/729	–	5.0	6.0	0.8	7	8	0.9	3	4	0.8
209	+	IPI00215637	DDX3X	ATP-dependent RNA helicase DDX3X	Non-raft	6	83/662	+	4.5	1.5	3.0	5	1	5.0	4	2	2.0
		IPI00215637	DDX3X	ATP-dependent RNA helicase DDX3X	Raft	4	52/662	–	2.0	2.0	1.0	3	3	1.0	1	1	1.0
210	–	IPI00017617	DDX5	Probable ATP-dependent RNA helicase DDX5	Non-raft	4	49/614	–	1.5	1.5	1.0	3	2	1.5	0	1	0.0
		IPI00017617	DDX5	Probable ATP-dependent RNA helicase DDX5	Raft	6	68/614	–	2.0	4.5	0.4	2	5	0.4	2	4	0.5
211	++	IPI00030320	DDX6	Probable ATP-dependent RNA helicase DDX6	Non-raft	2	26/483	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
		IPI00030320	DDX6	Probable ATP-dependent RNA helicase DDX6	Raft	3	42/483	+	1.5	0.5	3.0	2	0	6.7	1	1	1.0
212	+++	IPI00003482	DECR1	2,4-dienoyl-CoA reductase, mitochondrial precursor	Raft	5	72/335	+++	3.0	0.5	6.0	5	1	5.0	0	0	0.0
213	+	IPI00382990	DERP12	DERP12	Non-raft	12	134/343	+	11.5	7.0	1.6	14	9	1.6	9	5	1.8
		IPI00382990	DERP12	DERP12	Raft	28	286/343	+	64.5	39.5	1.6	74	55	1.3	55	24	2.3
214	+	IPI00294501	DHCR7	7-dehydrocholesterol reductase	Non-raft	3	32/475	+	2.0	1.0	2.0	3	2	1.5	1	0	3.3
215	–	IPI00396435	DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	Raft	7	86/795	–	4.5	3.5	1.3	8	6	1.3	1	1	1.0
216	–	IPI00411733	DHX30	Putative ATP-dependent RNA helicase DHX30	Non-raft	2	19/1194	–	0.0	1.0	0.0	0	1	0.0	0	1	0.0
217	–	IPI00027415	DHX36	Isoform 1 of Probable ATP-dependent RNA helicase DHX36	Raft	3	39/1008	–	1.0	1.5	0.7	2	3	0.7	0	0	0.0
218	–	IPI00844578	DHX9	ATP-dependent RNA helicase A	Non-raft	10	110/1270	–	4.5	4.5	1.0	8	6	1.3	1	3	0.3
		IPI00844578	DHX9	ATP-dependent RNA helicase A	Raft	18	250/1270	+	12.0	5.5	2.2	18	10	1.8	6	1	6.0
219	+	IPI00003269	DKFZp686D0972	hypothetical protein LOC345651	Raft	6	67/376	+	3.0	2.0	1.5	6	4	1.5	0	0	0.0
220	+++++	IPI00021338	DLAT	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor	Non-raft	8	108/614	+++++	8.0	1.5	5.3	7	1	7.0	9	2	4.5
		IPI00021338	DLAT	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor	Raft	5	77/614	++	3.5	1.0	3.5	4	1	4.0	3	1	3.0
221	–	IPI00015911	DLD	Dihydrolipoyl dehydrogenase, mitochondrial precursor	Non-raft	5	56/509	–	2.0	2.5	0.8	3	4	0.8	1	1	1.0
222	–	IPI00420108	DLST	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor	Non-raft	7	94/453	–	5.5	6.5	0.8	8	10	0.8	3	3	1.0
		IPI00420108	DLST	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor	Raft	9	105/453	+	10.5	6.0	1.8	16	9	1.8	5	3	1.7
223	–	IPI00012535	DNAJA1	DnaJ homolog subfamily A member 1	Non-raft	2	26/397	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
		IPI00012535	DNAJA1	DnaJ homolog subfamily A member 1	Raft	3	41/397	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
224	+	IPI00032406	DNAJA2	DnaJ homolog subfamily A member 2	Raft	3	52/412	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
225	–	IPI00178504	DNAJB14	DnaJ	Raft	2	23/379	–	0.5	0.5	1.0	1	0	3.3	0	1	0.0
226	+++++	IPI00023780	DNAJC5	Isoform 2 of DnaJ homolog subfamily C member 5	Non-raft	4	60/167	+++++	4.5	0.0	15.0	4	0	13.3	5	0	16.7

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
227	++++	IPI00402231	DNAJC5	Isoform 1 of DnaJ homolog subfamily C member 5	Non-raft	4	74/198	++++	5.0	0.0	16.7	6	0	20.0	4	0	13.3
228	-	IPI00329629	DNAJC7	DnaJ homolog subfamily C member 7	Non-raft	2	23/494	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
229	-	IPI00031519	DNMT1	Isoform 1 of DNA	Raft	3	30/1678	-	0.5	1.0	0.5	1	2	0.5	0	0	0.0
230	-	IPI00007425	DSC1	desmocollin 1 isoform Dsc1b preproprotein	Non-raft	2	29/840	-	0.0	1.0	0.0	0	2	0.0	0	0	0.0
231	-	IPI00025753	DSG1	Desmoglein-1 precursor	Non-raft	6	116/1049	-	0.0	5.5	0.0	0	9	0.0	0	2	0.0
		IPI00025753	DSG1	Desmoglein-1 precursor	Raft	5	84/1049	-	2.5	5.0	0.5	5	10	0.5	0	0	0.0
232	++++	IPI00028931	DSG2	desmoglein 2 preproprotein	Non-raft	25	396/1118	++++	33.0	1.5	22.0	36	2	18.0	30	1	30.0
		IPI00028931	DSG2	desmoglein 2 preproprotein	Raft	57	619/1118	++++	76.0	3.5	21.7	84	6	14.0	68	1	68.0
233	-	IPI00013933	DSP	Isoform DPI of Desmoplakin	Non-raft	11	136/2871	-	2.5	7.0	0.4	4	6	0.7	1	8	0.1
		IPI00013933	DSP	Isoform DPI of Desmoplakin	Raft	12	180/2871	+	6.0	2.0	3.0	11	4	2.8	1	0	3.3
234	-	IPI00473014	DSTN	Destrin	Non-raft	3	23/165	-	1.5	2.0	0.8	2	3	0.7	1	1	1.0
235	++	IPI00299076	EBAG9	Receptor-binding cancer antigen expressed on SiSo cells (Fragment)	Non-raft	2	50/213	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
236	++++	IPI00216760	ECE1	Isoform C of Endothelin-converting enzyme 1	Non-raft	20	300/754	++++	19.5	0.0	65.0	23	0	76.7	16	0	53.3
237	+	IPI00011416	ECH1	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor	Non-raft	6	72/328	+	3.0	1.5	2.0	4	1	4.0	2	2	1.0
238	+++	IPI00024993	ECHS1	Enoyl-CoA hydratase, mitochondrial precursor	Non-raft	2	35/290	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
239	++++	IPI00376317	EDC4	autoantigen RCD8	Raft	4	62/1401	++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0
240	+	IPI00306046	EDIL3	Isoform 1 of EGF-like repeat and discoidin I-like domain-containing protein 3 precursor	Non-raft	10	134/480	+	7.5	2.5	3.0	11	4	2.8	4	1	4.0
		IPI00306046	EDIL3	Isoform 1 of EGF-like repeat and discoidin I-like domain-containing protein 3 precursor	Raft	3	40/480	+	1.5	1.0	1.5	2	2	1.0	1	0	3.3
241	+	IPI00396485	EEF1A1	Elongation factor 1-alpha 1	Non-raft	18	275/462	+	23.5	9.5	2.5	21	14	1.5	26	5	5.2
		IPI00396485	EEF1A1	Elongation factor 1-alpha 1	Raft	11	156/462	+	10.0	5.5	1.8	15	6	2.5	5	5	1.0
242	+	IPI00014424	EEF1A2	Elongation factor 1-alpha 2	Non-raft	11	138/463	+	12.0	4.5	2.7	10	4	2.5	14	5	2.8
		IPI00014424	EEF1A2	Elongation factor 1-alpha 2	Raft	8	124/463	-	5.5	5.0	1.1	5	6	0.8	6	4	1.5
243	++	IPI00023048	EEF1D	Elongation factor 1-delta	Non-raft	2	28/281	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
		IPI00023048	EEF1D	Elongation factor 1-delta	Raft	6	64/281	+	5.0	2.0	2.5	6	3	2.0	4	1	4.0
244	-	IPI00000875	EEF1G	Elongation factor 1-gamma	Non-raft	8	86/487	-	6.5	7.0	0.9	8	7	1.1	5	7	0.7
		IPI00000875	EEF1G	Elongation factor 1-gamma	Raft	17	211/487	-	11.5	10.0	1.2	14	15	0.9	9	5	1.8
245	+	IPI00186290	EEF2	Elongation factor 2	Non-raft	28	355/858	+	26.5	17.0	1.6	34	22	1.5	19	12	1.6
		IPI00186290	EEF2	Elongation factor 2	Raft	5	64/858	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
246	++++	IPI00304661	EEPD1	hypothetical protein LOC80820	Raft	6	82/157	++++	3.0	0.0	10.0	2	0	6.7	4	0	13.3
247	+++++	IPI00470711	EFR3A	Hypothetical protein DKFZp781J0562	Non-raft	10	128/821	+++++	6.5	0.0	21.7	7	0	23.3	6	0	20.0
		IPI00470711	EFR3A	Hypothetical protein DKFZp781J0562	Raft	7	81/821	+++++	4.0	0.0	13.3	3	0	10.0	5	0	16.7
248	-	IPI00003519	EFTUD2	116 kDa U5 small nuclear ribonucleoprotein component	Raft	5	62/972	-	1.0	1.5	0.7	2	3	0.7	0	0	0.0
249	-	IPI00018274	EGFR	Isoform 1 of Epidermal growth factor receptor precursor	Non-raft	13	169/1210	-	4.5	7.0	0.6	5	11	0.5	4	3	1.3
250	-	IPI00012462	EIF2A	CDA02	Raft	6	99/609	-	2.5	2.5	1.0	5	5	1.0	0	0	0.0
251	+	IPI00220349	EIF2C2	eukaryotic translation initiation factor 2C, 2	Raft	4	48/859	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
252	-	IPI00219678	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	Non-raft	4	48/315	-	1.0	3.0	0.3	2	4	0.5	0	2	0.0
		IPI00219678	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	Raft	8	116/315	-	3.5	3.0	1.2	6	5	1.2	1	1	1.0
253	-	IPI00297982	EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	Non-raft	7	99/472	+	4.5	3.0	1.5	8	3	2.7	1	3	0.3
		IPI00297982	EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	Raft	11	178/472	-	10.0	7.0	1.4	15	10	1.5	5	4	1.3
254	-	IPI00396370	EIF3B	Isoform 1 of Eukaryotic translation initiation factor 3 subunit 9	Non-raft	3	37/814	-	1.0	1.0	1.0	2	2	1.0	0	0	0.0
		IPI00396370	EIF3B	Isoform 1 of Eukaryotic translation initiation factor 3 subunit 9	Raft	2	23/814	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
255	+++	IPI00016910	EIF3C	Eukaryotic translation initiation factor 3 subunit 8	Non-raft	4	45/913	+++	2.0	0.0	6.7	3	0	10.0	1	0	3.3
256	+	IPI00006181	EIF3D	Eukaryotic translation initiation factor 3 subunit 7	Non-raft	3	34/548	–	2.0	1.5	1.3	4	3	1.3	0	0	0.0
		IPI00006181	EIF3D	Eukaryotic translation initiation factor 3 subunit 7	Raft	4	52/548	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
257	+	IPI00465233	EIF3EIP	DJ1014D13.1 protein	Non-raft	3	37/607	+	2.0	1.0	2.0	3	1	3.0	1	1	1.0
258	++	IPI00654777	EIF3F	Eukaryotic translation initiation factor 3 subunit 5	Raft	2	30/372	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
259	++	IPI00290460	EIF3G	Eukaryotic translation initiation factor 3 subunit 4	Raft	2	25/320	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
260	+++	IPI00647650	EIF3H	Eukaryotic translation initiation factor 3 subunit 3	Raft	3	50/366	+++	2.5	0.5	5.0	3	1	3.0	2	0	6.7
261	+	IPI00012795	EIF3I	Eukaryotic translation initiation factor 3 subunit 2	Non-raft	9	124/325	+	3.5	1.5	2.3	6	3	2.0	1	0	3.3
		IPI00012795	EIF3I	Eukaryotic translation initiation factor 3 subunit 2	Raft	3	33/325	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
262	+++	IPI00033143	EIF3K	Eukaryotic translation initiation factor 3 subunit 12	Non-raft	2	28/218	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
		IPI00033143	EIF3K	Eukaryotic translation initiation factor 3 subunit 12	Raft	4	43/218	+++	3.0	0.5	6.0	5	1	5.0	1	0	3.3
263	+	IPI00025491	EIF4A1	Eukaryotic initiation factor 4A-I	Non-raft	7	104/406	+	7.5	2.5	3.0	11	4	2.8	4	1	4.0
		IPI00025491	EIF4A1	Eukaryotic initiation factor 4A-I	Raft	4	47/406	+	2.5	1.5	1.7	3	3	1.0	2	0	6.7
264	+	IPI00009328	EIF4A3	Probable ATP-dependent RNA helicase DDX48	Raft	4	51/411	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
265	+	IPI00220365	EIF4G1	EIF4G1 variant protein (Fragment)	Non-raft	3	33/798	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
266	++++	IPI00022648	EIF5	Eukaryotic translation initiation factor 5	Non-raft	4	35/431	++++	2.5	0.0	8.3	3	0	10.0	2	0	6.7
267	+++	IPI00006935	EIF5A2	Eukaryotic translation initiation factor 5A-2	Raft	2	19/153	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
268	++	IPI00010105	EIF6	Eukaryotic translation initiation factor 6	Non-raft	2	32/245	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00010105	EIF6	Eukaryotic translation initiation factor 6	Raft	3	67/245	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
269	–	IPI00301936	ELAVL1	ELAV-like protein 1	Non-raft	3	33/353	–	1.5	1.5	1.0	3	2	1.5	0	1	0.0
		IPI00301936	ELAVL1	ELAV-like protein 1	Raft	8	94/353	+	4.0	2.5	1.6	6	5	1.2	2	0	6.7
270	+++++	IPI00010187	ELOVL1	Elongation of very long chain fatty acids protein 1	Non-raft	2	25/279	+++++	5.0	0.5	10.0	7	1	7.0	3	0	10.0
271	–	IPI00465248	ENO1	enolase 1	Non-raft	17	249/434	–	11.0	10.0	1.1	15	15	1.0	7	5	1.4
		IPI00465248	ENO1	enolase 1	Raft	2	23/434	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
272	+	IPI00218474	ENO3	Beta-enolase	Non-raft	4	81/434	+	3.5	1.5	2.3	6	3	2.0	1	0	3.3
273	–	IPI00015973	EPB41L2	Band 4.1-like protein 2	Non-raft	2	27/1005	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
274	–	IPI00021267	EPHA2	Ephrin type-A receptor 2 precursor	Non-raft	13	141/976	–	5.5	5.5	1.0	9	8	1.1	2	3	0.7
		IPI00021267	EPHA2	Ephrin type-A receptor 2 precursor	Raft	2	18/976	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
275	–	IPI00186826	EPHB4	Receptor protein tyrosine kinase variant EphB4v1	Non-raft	3	30/935	–	1.0	1.5	0.7	2	3	0.7	0	0	0.0
276	+	IPI00013452	EPRS	glutamyl-prolyl tRNA synthetase	Non-raft	8	106/1512	+	3.0	1.5	2.0	6	3	2.0	0	0	0.0
		IPI00013452	EPRS	glutamyl-prolyl tRNA synthetase	Raft	2	22/1512	–	0.5	0.5	1.0	1	1	1			

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
288	–	IPI00001754	F11R	Junctional adhesion molecule A precursor	Non-raft	4	58/299	–	1.5	2.0	0.8	3	4	0.8	0	0	0.0
289	+++++	IPI00010338	F3	Tissue factor precursor	Non-raft	6	75/295	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
290	+++++	IPI00412592	FAM108B1	chromosome 9 open reading frame 77 isoform 2	Non-raft	8	144/288	+++++	5.5	0.0	18.3	8	0	26.7	3	0	10.0
		IPI00412592	FAM108B1	chromosome 9 open reading frame 77 isoform 2	Raft	2	26/288	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
291	++	IPI00747290	FAM108C1	Isoform 2 of abhydrolase domain-containing protein FAM108C1	Non-raft	2	22/295	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
292	++	IPI00039626	FAM120A	Isoform D of UPF0318 protein FAM120A	Raft	4	60/1072	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
293	+	IPI00456750	FAM129B	Niban-like protein	Non-raft	2	24/733	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
294	++	IPI00021923	FAM3C	Protein FAM3C precursor	Non-raft	2	22/227	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
295	+++++	IPI00303318	FAM49B	Protein FAM49B	Non-raft	20	241/324	+++++	25.0	0.0	83.3	31	0	103.3	19	0	63.3
		IPI00303318	FAM49B	Protein FAM49B	Raft	2	37/324	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
296	–	IPI00022143	FAM62A	Isoform 1 of Protein FAM62A	Non-raft	11	163/1104	–	5.0	4.5	1.1	6	5	1.2	4	4	1.0
297	–	IPI00300074	FARSB	Phenylalanyl-tRNA synthetase beta chain	Non-raft	8	92/589	–	3.5	3.5	1.0	3	4	0.8	4	3	1.3
		IPI00300074	FARSB	Phenylalanyl-tRNA synthetase beta chain	Raft	10	110/589	–	5.5	4.5	1.2	8	4	2.0	3	5	0.6
298	+++++	IPI00026781	FASN	Fatty acid synthase	Non-raft	41	545/2511	+++++	25.5	5.5	4.6	31	8	3.9	20	3	6.7
		IPI00026781	FASN	Fatty acid synthase	Raft	3	32/2511	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
299	++++	IPI00174757	FBXL20	F-box/LRR-repeat protein 20	Non-raft	5	53/436	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
300	+++++	IPI00021048	FER1L3	Isoform 1 of Myoferlin	Non-raft	91	956/2061	++	80.0	22.5	3.6	94	32	2.9	66	13	5.1
		IPI00021048	FER1L3	Isoform 1 of Myoferlin	Raft	21	275/2061	+++++	15.5	1.5	10.3	22	3	7.3	9	0	30.0
301	+	IPI00000856	FERMT2	Isoform 1 of Pleckstrin homology domain-containing family C member 1	Non-raft	3	42/680	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
302	–	IPI00328161	FKBP8	FK506-binding protein 8	Non-raft	5	87/413	–	1.5	2.5	0.6	1	2	0.5	2	3	0.7
303	++	IPI00013281	FKRP	Fukutin-related protein	Non-raft	2	25/495	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
304	–	IPI00397801	FLG2	Ifapsoriasis	Non-raft	2	23/2391	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
		IPI00397801	FLG2	Ifapsoriasis	Raft	2	23/2391	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
305	+++	IPI00301987	FLJ20323	hypothetical protein FLJ20323	Raft	5	73/875	+++	2.5	0.5	5.0	5	1	5.0	0	0	0.0
306	–	IPI00302592	FLNA	filamin 1	Non-raft	79	1117/2639	–	37.0	44.5	0.8	53	63	0.8	21	26	0.8
		IPI00302592	FLNA	filamin 1	Raft	29	452/2639	–	12.5	11.0	1.1	25	21	1.2	0	1	0.0
307	–	IPI00477536	FLNB	Filamin B	Non-raft	83	1102/2591	–	38.5	45.0	0.9	54	68	0.8	23	22	1.0
		IPI00477536	FLNB	Filamin B	Raft	23	312/2591	–	8.0	7.0	1.1	16	14	1.1	0	0	0.0
308	–	IPI00178352	FLNC	Isoform 1 of Filamin-C	Non-raft	23	276/2725	–	6.5	7.0	0.9	11	13	0.8	3	1	3.0
		IPI00178352	FLNC	Isoform 1 of Filamin-C	Raft	4	52/2725	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
309	+++++	IPI00027438	FLOT1	Flotillin-1	Non-raft	25	303/427	+++++	25.5	0.5	51.0	27	1	27.0	24	0	80.0
		IPI00027438	FLOT1	Flotillin-1	Raft	33	351/427	+++++	50.5	3.0	16.8	52	4	13.0	49	2	24.5
310	+++++	IPI00029625	FLOT2	Flotillin-2	Non-raft	24	260/428	+++++	32.0	0.5	64.0	34	1	34.0	30	0	100.0
		IPI00029625	FLOT2	Flotillin-2	Raft	33	404/428	+++++	56.0	2.5	22.4	60	5	12.0	52	0	173.3
311	–	IPI00217490	FNDC3B	Factor for adipocyte differentiation 104 variant	Non-raft	2	23/1204	–	0.0	1.5	0.0	0	2	0.0	0	1	0.0
		IPI00217490	FNDC3B	Factor for adipocyte differentiation 104 variant	Raft	5	73/1204	–	1.5	1.5	1.0	3	3	1.0	0	0	0.0
312	+	IPI00163187	FSCN1	Fascin	Non-raft	8	116/493	+	5.0	2.0	2.5	8	3	2.7	2	1	2.0
313	–	IPI00016249	FXR1	Isoform 1 of Fragile X mental retardation syndrome-related protein 1	Raft	6	76/621	–	2.5	2.5	1.0	5	4	1.3	0	1	0.0
314	++	IPI00016250	FXR2	Fragile X mental retardation syndrome-related protein 2	Raft	3	43/698	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
315	+++++	IPI00020228	FZD6	Frizzled-6 precursor	Non-raft	3	28/706	+++++	3.0	0.0	10.0	3	0	10.0	3	0	10.0
316	–	IPI00012442	G3BP1	Ras-GTPase-activating protein-binding protein 1	Raft	7	102/466	–	2.0	2.5	0.8	4	5	0.8	0	0	0.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
317	–	IPI00216008	G6PD	Isoform Long of Glucose-6-phosphate 1-dehydrogenase	Non-raft	4	43/561	–	1.5	2.0	0.8	2	3	0.7	1	1	1.0
318	+	IPI00004669	GALNT2	Polypeptide N-acetylgalactosaminyltransferase 2	Non-raft	5	62/571	+	2.0	1.0	2.0	4	1	4.0	0	1	0.0
319	+	IPI00011454	GANAB	Isoform 2 of Neutral alpha-glucosidase AB precursor	Non-raft	14	216/966	+	7.5	4.0	1.9	12	7	1.7	3	1	3.0
320	+++++	IPI00219018	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	Non-raft	29	361/335	+	122.0	52.5	2.3	143	62	2.3	101	43	2.3
		IPI00219018	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	Raft	12	160/335	+++++	13.5	4.0	3.4	15	5	3.0	12	3	4.0
321	–	IPI00465260	GARS	GARS protein	Non-raft	9	158/739	–	4.0	3.0	1.3	5	4	1.3	3	2	1.5
322	++	IPI00025273	GART	Isoform Long of Trifunctional purine biosynthetic protein adenosine-3	Non-raft	2	27/1010	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
323	+	IPI00021807	GBA	Isoform Long of Glucosylceramidase precursor	Non-raft	4	58/536	+	2.0	1.0	2.0	2	1	2.0	2	1	2.0
324	–	IPI00001159	GCN1L1	GCN1-like protein 1	Non-raft	8	94/2671	–	3.0	3.5	0.9	4	6	0.7	2	1	2.0
325	–	IPI00031461	GDI2	Rab GDP dissociation inhibitor beta	Non-raft	3	42/449	–	0.5	1.5	0.3	1	3	0.3	0	0	0.0
326	+	IPI00154473	GFM1	84 kDa protein	Non-raft	4	39/751	+	1.5	1.0	1.5	2	2	1.0	1	0	3.3
327	+++++	IPI00217952	GFPT1	Isoform 1 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	Non-raft	10	140/699	+++++	6.5	0.0	21.7	7	0	23.3	6	0	20.0
328	–	IPI00414717	GLG1	golgi apparatus protein 1	Non-raft	9	97/1203	–	4.0	3.0	1.3	5	2	2.5	3	4	0.8
329	–	IPI00215687	GLS	Isoform GAC of Glutaminase kidney isoform, mitochondrial precursor	Non-raft	12	194/598	–	13.5	10.0	1.4	12	9	1.3	15	11	1.4
330	–	IPI00289159	GLS	Isoform KGA of Glutaminase kidney isoform, mitochondrial precursor	Non-raft	13	171/669	–	12.5	9.5	1.3	11	9	1.2	14	10	1.4
331	–	IPI00168262	GLT25D1	CDNA PSEC0241 fis, clone NT2RP3000234, moderately similar to Homo sapiens cerebral cell adhesion molecule mRNA	Non-raft	2	18/622	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
		IPI00168262	GLT25D1	CDNA PSEC0241 fis, clone NT2RP3000234, moderately similar to Homo sapiens cerebral cell adhesion molecule mRNA	Raft	2	18/622	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
332	–	IPI00016801	GLUD1	Glutamate dehydrogenase 1, mitochondrial precursor	Raft	9	110/558	–	8.0	8.0	1.0	9	11	0.8	7	5	1.4
333	+++++	IPI00305551	GNA11	Guanine nucleotide-binding protein subunit alpha-11	Non-raft	24	278/359	+++++	28.0	1.0	28.0	36	1	36.0	20	1	20.0
		IPI00305551	GNA11	Guanine nucleotide-binding protein subunit alpha-11	Raft	13	155/359	+++++	10.5	0.0	35.0	11	0	36.7	10	0	33.3
334	+++++	IPI00328744	GNA12	Guanine nucleotide-binding protein alpha-12 subunit	Non-raft	6	71/381	+++++	8.5	0.0	28.3	9	0	30.0	8	0	26.7
335	+++++	IPI00290928	GNA13	Guanine nucleotide-binding protein alpha-13 subunit	Non-raft	17	194/377	+++++	22.5	1.0	22.5	26	1	26.0	19	1	19.0
		IPI00290928	GNA13	Guanine nucleotide-binding protein alpha-13 subunit	Raft	7	102/377	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
336	+++++	IPI00337415	GNAI1	Guanine nucleotide-binding protein G(i), alpha-1 subunit	Non-raft	14	161/354	+++++	12.0	1.0	12.0	13	0	43.3	11	2	5.5
		IPI00337415	GNAI1	Guanine nucleotide-binding protein G(i), alpha-1 subunit	Raft	12	134/354	+++++	11.0	0.0	36.7	10	0	33.3	12	0	40.0
337	+++++	IPI00748145	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	Non-raft	23	248/355	+++++	31.0	5.0	6.2	40	5	8.0	22	5	4.4
		IPI00748145	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	Raft	20	230/355	+++++	23.0	1.0	23.0	18	1	18.0	28	1	28.0
338	+++++	IPI00220578	GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha	Non-raft	19	234/354	+++++	28.5	5.0	5.7	32	4	8.0	25	6	4.2
		IPI00220578	GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha	Raft	16	206/354	+++++	17.5	0.5	35.0	14	0	46.7	21	1	21.0
339	++++	IPI00220281	GNAO1	Guanine nucleotide-binding protein G(o) subunit alpha 1	Non-raft	5	52/354	++++	3.0	0.0	10.0	6	0	20.0	0	0	0.0
340	+++++	IPI00288947	GNAQ	Guanine nucleotide binding protein	Non-raft	19	262/359	+++++	21.5	0.5	43.0	22	0	73.3	21	1	21.0
		IPI00288947	GNAQ	Guanine nucleotide binding protein	Raft	13	212/359	+++++	12.5	0.0	41.7	13	0	43.3	12	0	40.0
341	+++++	IPI00219835	GNAS	Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	Non-raft	19	236/380	+++++	25.5	3.5	7.3	34	6	5.7	17	1	17.0
		IPI00219835	GNAS	Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	Raft	22	256/380	+++++	19.0	0.0	63.3	18	0	60.0	20	0	66.7

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
342	+++++	IPI00514055	GNAS	Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	Non-raft	18	229/394	+++++	24.5	3.5	7.0	30	6	5.0	19	1	19.0
		IPI00514055	GNAS	Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	Raft	22	261/394	+++++	20.0	0.0	66.7	18	0	60.0	22	0	73.3
343	+++++	IPI00644936	GNAS	Guanine nucleotide-binding protein G-s-alpha-3	Raft	22	258/379	+++++	18.5	0.0	61.7	17	0	56.7	20	0	66.7
344	–	IPI00026268	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	Non-raft	9	145/340	–	6.0	6.0	1.0	11	9	1.2	1	3	0.3
		IPI00026268	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	Raft	6	74/340	+	2.5	1.5	1.7	4	2	2.0	1	1	1.0
345	+	IPI00003348	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2	Non-raft	8	95/340	–	3.5	5.0	0.7	5	6	0.8	2	4	0.5
		IPI00003348	GNB2	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2	Raft	6	74/340	+++	3.0	0.5	6.0	4	1	4.0	2	0	6.7
346	+	IPI00641950	GNB2L1	Lung cancer oncogene 7	Non-raft	9	102/347	–	5.5	5.0	1.1	4	6	0.7	7	4	1.8
		IPI00641950	GNB2L1	Lung cancer oncogene 7	Raft	20	243/347	+	31.5	19.5	1.6	38	25	1.5	25	14	1.8
347	–	IPI00012451	GNB4	Guanine nucleotide-binding protein subunit beta 4	Non-raft	5	60/340	–	2.0	2.5	0.8	4	5	0.8	0	0	0.0
348	+	IPI00005677	GNPAT	Dihydroxyacetone phosphate acyltransferase	Non-raft	2	22/680	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
349	+++++	IPI00480022	GOLGA7	Isoform 1 of Golgin subfamily A member 7	Non-raft	8	98/137	+++++	7.0	0.0	23.3	8	0	26.7	6	0	20.0
		IPI00480022	GOLGA7	Isoform 1 of Golgin subfamily A member 7	Raft	10	108/137	+++++	7.5	0.5	15.0	10	1	10.0	5	0	16.7
350	+++++	IPI00004962	GOLIM4	golgi phosphoprotein 4	Non-raft	9	116/696	+++++	6.5	0.0	21.7	9	0	30.0	4	0	13.3
351	–	IPI00018206	GOT2	Aspartate aminotransferase, mitochondrial precursor	Non-raft	11	142/430	–	4.5	5.0	0.9	5	6	0.8	4	4	1.0
352	++++	IPI00027497	GPI	Glucose-6-phosphate isomerase	Non-raft	3	43/558	++++	4.5	0.5	9.0	7	1	7.0	2	0	6.7
353	+++++	IPI00217481	GPR126	Developmentally regulated G-protein-coupled receptor beta 1	Non-raft	7	97/1250	+++++	5.5	0.0	18.3	6	0	20.0	5	0	16.7
		IPI00217481	GPR126	Developmentally regulated G-protein-coupled receptor beta 1	Raft	4	53/1250	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
354	+++++	IPI00022624	GPRC5A	Retinoic acid-induced protein 3	Non-raft	7	95/357	+++++	15.0	0.5	30.0	17	1	17.0	13	0	43.3
		IPI00022624	GPRC5A	Retinoic acid-induced protein 3	Raft	10	135/357	+++++	23.0	1.0	23.0	31	2	15.5	15	0	50.0
355	++++	IPI00099883	GPRC5C	G-protein coupled receptor family C group 5 member C precursor	Raft	6	51/441	++++	4.5	0.0	15.0	9	0	30.0	0	0	0.0
356	++	IPI00332155	GPRIN1	Isoform 1 of G protein-regulated inducer of neurite outgrowth 1	Non-raft	2	30/1008	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
357	–	IPI00027831	GRWD1	Glutamate-rich WD repeat-containing protein 1	Raft	2	30/446	–	0.0	1.0	0.0	0	2	0.0	0	0	0.0
358	+	IPI00016862	GSR	Isoform Mitochondrial of Glutathione reductase, mitochondrial precursor	Non-raft	3	43/522	+	1.5	1.0	1.5	2	2	1.0	1	0	3.3
359	–	IPI00031522	HADHA	Trifunctional enzyme subunit alpha, mitochondrial precursor	Non-raft	17	230/763	–	10.5	7.5	1.4	13	11	1.2	8	4	2.0
		IPI00031522	HADHA	Trifunctional enzyme subunit alpha, mitochondrial precursor	Raft	12	154/763	+	6.0	4.0	1.5	9	7	1.3	3	1	3.0
360	+	IPI00022793	HADHB	Trifunctional enzyme beta subunit, mitochondrial precursor	Non-raft	2	18/474	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
		IPI00022793	HADHB	Trifunctional enzyme beta subunit, mitochondrial precursor	Raft	2	18/474	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
361	–	IPI00654755	HBB	Hemoglobin subunit beta	Non-raft	2	23/147	–	0.0	1.5	0.0	0	0	0.0	0	3	0.0
		IPI00654755	HBB	Hemoglobin subunit beta	Raft	2	22/147	–	0.5	1.0	0.5	1	1	1.0	0	1	0.0
362	+	IPI00176692	hCG_2023776	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1	Non-raft	3	59/281	++	2.0	0.5	4.0	2	1	2.0	2	0	6.7
		IPI00176692	hCG_2023776	PREDICTED: similar to Heterogeneous nuclear ribonucleoprotein A1	Raft	5	73/281	+	2.0	1.0	2.0	4	2	2.0	0	0	0.0
363	–	IPI00022228	HDLBP	Vigilin	Raft	5	70/1268	–	1.0	2.0	0.5	2	4	0.5	0	0	0.0
364	–	IPI00453473	HIST1H4A	Histone H4	Non-raft	2	20/103	–	0.0	1.0	0.0	0	2	0.0	0	0	0.0
365	–	IPI00018246	HK1	Isoform 1 of Hexokinase-1	Non-raft	7	91/917	–	2.5	3.5	0.7	2	3	0.7	3	4	0.8
366	+	IPI00743503	HLA-A	HLA class I histocompatibility antigen, A-34 alpha chain precursor	Non-raft	11	162/365	+	32.5	11.0	3.0	33	16	2.1	32	6	5.3
367	+++++	IPI00471955	HLA-B	HLA class I histocompatibility antigen, B-50 alpha chain precursor	Non-raft	16	262/362	+++++	54.5	10.0	5.5	54	13	4.2	55	7	7.8

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
		IPI00471955	HLA-B	HLA class I histocompatibility antigen, B-50 alpha chain precursor	Raft	8	101/362	+++++	11.0	1.5	7.3	11	3	3.7	11	0	36.7
368	+++++	IPI00473131	HLA-C	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	Non-raft	18	241/366	+++++	43.5	12.5	3.5	44	17	2.6	43	8	5.4
		IPI00473131	HLA-C	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	Raft	11	154/366	+++++	12.0	1.5	8.0	13	3	4.3	11	0	36.7
369	+++++	IPI00008475	HMGCS1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	Non-raft	8	134/520	+++++	6.5	0.0	21.7	9	0	30.0	4	0	13.3
370	+	IPI00026824	HMOX2	Heme oxygenase 2	Non-raft	7	118/370	+	4.0	2.0	2.0	4	4	1.0	4	0	13.3
371	+++	IPI00011913	HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0	Raft	2	33/305	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
372	+	IPI00215965	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1 isoform b	Non-raft	4	77/372	+	2.5	1.0	2.5	3	2	1.5	2	0	6.7
		IPI00215965	HNRNPA1	heterogeneous nuclear ribonucleoprotein A1 isoform b	Raft	7	102/372	+	5.0	2.5	2.0	9	5	1.8	1	0	3.3
373	+	IPI00396378	HNRNPA2B1	Isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1	Raft	3	34/353	+	1.5	0.5	3.0	2	1	2.0	0	0	0.0
374	–	IPI00027834	HNRNPL	heterogeneous nuclear ribonucleoprotein L isoform a	Raft	9	190/589	–	4.5	4.0	1.1	8	6	1.3	1	2	0.5
375	–	IPI00012074	HNRNPR	Heterogeneous nuclear ribonucleoprotein R	Raft	3	33/633	–	1.5	2.5	0.6	3	5	0.6	0	0	0.0
376	–	IPI00479217	HNRNPU	heterogeneous nuclear ribonucleoprotein U isoform b	Non-raft	6	59/806	–	2.0	4.0	0.5	4	3	1.3	0	1	0.0
377	+++	IPI00419373	HNRPA3	Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	Raft	4	71/378	+++	2.5	0.5	5.0	4	1	4.0	1	0	3.3
378	+	IPI00028888	HNRPD	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	Raft	2	24/355	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
379	+	IPI00003881	HNRPF	heterogeneous nuclear ribonucleoprotein F	Non-raft	2	34/415	+	1.5	0.5	3.0	1	1	1.0	2	0	6.7
380	–	IPI00013881	HNRPH1	heterogeneous nuclear ribonucleoprotein H1	Non-raft	2	34/449	–	0.5	1.0	0.5	0	1	0.0	1	1	1.0
		IPI00013881	HNRPH1	heterogeneous nuclear ribonucleoprotein H1	Raft	2	33/449	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
381	–	IPI00216049	HNRPK	Isoform 1 of Heterogeneous nuclear ribonucleoprotein K	Non-raft	10	127/463	–	5.0	3.5	1.4	6	4	1.5	4	3	1.3
		IPI00216049	HNRPK	Isoform 1 of Heterogeneous nuclear ribonucleoprotein K	Raft	8	121/463	–	3.5	2.5	1.4	5	3	1.7	2	2	1.0
382	++	IPI00171903	HNRPM	heterogeneous nuclear ribonucleoprotein M isoform a	Non-raft	5	70/730	+	2.5	1.5	1.7	3	2	1.5	2	1	2.0
		IPI00171903	HNRPM	heterogeneous nuclear ribonucleoprotein M isoform a	Raft	13	146/730	+++	7.5	1.5	5.0	13	1	13.0	2	2	1.0
383	+++++	IPI00000006	HRAS	GTPase HRas precursor	Non-raft	9	85/189	+++++	11.0	0.5	22.0	9	0	30.0	13	1	13.0
384	+	IPI00398625	HRNR	Hornerin	Non-raft	4	66/2850	+	2.0	1.0	2.0	4	2	2.0	0	0	0.0
		IPI00398625	HRNR	Hornerin	Raft	11	196/2850	+	7.5	3.5	2.1	15	7	2.1	0	0	0.0
385	+++++	IPI00017726	HSD17B10	hydroxyacyl-Coenzyme A dehydrogenase, type II isoform 1	Non-raft	5	88/261	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
386	+	IPI00019912	HSD17B4	Peroxisomal multifunctional enzyme type 2	Non-raft	11	147/736	+	6.0	3.0	2.0	8	5	1.6	4	1	4.0
387	–	IPI00382470	HSP90AA1	Heat shock protein HSP 90-alpha 2	Non-raft	14	163/854	–	11.5	10.5	1.1	15	15	1.0	8	6	1.3
		IPI00382470	HSP90AA1	Heat shock protein HSP 90-alpha 2	Raft	9	118/854	–	3.5	5.0	0.7	7	10	0.7	0	0	0.0
388	–	IPI00414676	HSP90AB1	Heat shock protein HSP 90-beta	Non-raft	24	284/724	–	16.5	16.5	1.0	23	24	1.0	10	9	1.1
		IPI00414676	HSP90AB1	Heat shock protein HSP 90-beta	Raft	7	88/724	–	2.0	2.5	0.8	4	5	0.8	0	0	0.0
389	–	IPI00555915	HSP90AB6P	Heat shock protein 90Bf	Non-raft	2	20/361	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
390	–	IPI00027230	HSP90B1	Endoplasmin precursor	Non-raft	17	204/803	–	10.0	7.5	1.3	14	11	1.3	6	4	1.5
391	+	IPI00304925	HSPA1A	Heat shock 70 kDa protein 1	Non-raft	8	96/641	–	3.5	4.5	0.8	4	6	0.7	3	4	0.8
		IPI00304925	HSPA1A	Heat shock 70 kDa protein 1	Raft	3	40/641	+++	1.5	0.0	5.0	0	0	0.0	3	0	10.0
392	–	IPI00301277	HSPA1L	Heat shock 70 kDa protein 1L	Non-raft	7	87/641	–	3.5	4.0	0.9	4	5	0.8	3	3	1.0
		IPI00301277	HSPA1L	Heat shock 70 kDa protein 1L	Raft	2	31/641	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
393	–	IPI00002966	HSPA4	Heat shock 70 kDa protein 4	Non-raft	8	101/840	–	4.0	3.0	1.3	7	4	1.8	1	1	1.0
394	–	IPI00003362	HSPA5	Hypothetical protein	Non-raft	29	309/655	–	28.0	28.0	1.0	35	36	1.0	21	20	1.1
		IPI00003362	HSPA5	Hypothetical protein	Raft	11	141/655	–	6.5	5.0	1.3	7	6	1.2	6	4	1.5
395	+	IPI00003865	HSPA8	Isoform 1 of Heat shock cognate 71 kDa protein	Non-raft	19	235/646	+	15.5	9.5	1.6	21	13	1.6	10	6	1.7
		IPI00003865	HSPA8	Isoform 1 of Heat shock cognate 71 kDa protein	Raft	13	167/646	+	5.0	2.5	2.0	4	3	1.3	6	2	3.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
396	–	IPI00007765	HSPA9	Stress-70 protein, mitochondrial precursor	Non-raft	19	275/679	–	12.0	19.0	0.6	16	25	0.6	8	13	0.6
		IPI00007765	HSPA9	Stress-70 protein, mitochondrial precursor	Raft	15	197/679	–	7.0	7.0	1.0	8	10	0.8	6	4	1.5
397	+	IPI00472102	HSPD1	Heat shock protein 60	Non-raft	23	264/573	+	23.5	12.0	2.0	30	16	1.9	17	8	2.1
398	–	IPI00024284	HSPG2	Basement membrane-specific heparan sulfate proteoglycan core protein precursor	Raft	4	50/4391	–	0.0	2.0	0.0	0	4	0.0	0	0	0.0
399	–	IPI00218993	HSPH1	Isoform Beta of Heat-shock protein 105 kDa	Non-raft	5	65/814	–	2.0	1.5	1.3	4	2	2.0	0	1	0.0
400	+	IPI00013234	IARS	IARS protein	Non-raft	4	43/1266	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
401	–	IPI00008494	ICAM1	Intercellular adhesion molecule 1 precursor	Non-raft	11	117/532	–	5.0	5.5	0.9	9	8	1.1	1	3	0.3
402	–	IPI00030702	IDH3A	Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor	Non-raft	2	18/366	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
403	++++	IPI00289819	IGF2R	Cation-independent mannose-6-phosphate receptor precursor	Non-raft	11	135/2491	+	5.5	3.5	1.6	7	6	1.2	4	1	4.0
		IPI00289819	IGF2R	Cation-independent mannose-6-phosphate receptor precursor	Raft	10	108/2491	++++	5.0	0.0	16.7	10	0	33.3	0	0	0.0
404	+++	IPI00056478	IGSF8	Isoform 1 of Immunoglobulin superfamily member 8 precursor	Non-raft	3	40/613	+++	2.0	0.0	6.7	1	0	3.3	3	0	10.0
405	+++	IPI00788962	IL10RB	Protein	Non-raft	2	23/292	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
406	++	IPI00006774	IL27RA	Interleukin-27 receptor subunit alpha	Non-raft	2	37/725	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
407	+++	IPI00297124	IL6ST	Isoform 1 of Interleukin-6 receptor beta chain precursor	Non-raft	2	27/918	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
408	–	IPI00005198	ILF2	Interleukin enhancer-binding factor 2	Non-raft	2	24/390	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
		IPI00005198	ILF2	Interleukin enhancer-binding factor 2	Raft	4	56/390	+	2.5	1.5	1.7	2	2	1.0	3	1	3.0
409	+	IPI00219330	ILF3	Isoform 5 of Interleukin enhancer-binding factor 3	Non-raft	3	39/690	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
		IPI00219330	ILF3	Isoform 5 of Interleukin enhancer-binding factor 3	Raft	8	92/690	–	3.0	3.0	1.0	6	6	1.0	0	0	0.0
410	+++	IPI00554541	ILVBL	ilvB (bacterial acetolactate synthase)-like isoform 1	Non-raft	3	49/632	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
411	+	IPI00291510	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	Non-raft	2	31/514	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
		IPI00291510	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	Raft	6	92/514	–	2.0	2.0	1.0	2	4	0.5	2	0	6.7
412	++	IPI00032262	INPP5A	Type I inositol-1,4,5-trisphosphate 5-phosphatase	Raft	2	19/412	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
413	–	IPI00009342	IQGAP1	Ras GTPase-activating-like protein IQGAP1	Non-raft	4	50/1657	–	0.5	2.5	0.2	1	4	0.3	0	1	0.0
414	–	IPI00013744	ITGA2	Integrin alpha-2 precursor	Non-raft	10	133/1181	–	5.0	3.5	1.4	7	4	1.8	3	2	1.5
415	++	IPI00215995	ITGA3	Isoform Alpha-3A of Integrin alpha-3 precursor	Non-raft	14	166/1051	++	15.5	4.5	3.4	15	7	2.1	16	2	8.0
		IPI00215995	ITGA3	Isoform Alpha-3A of Integrin alpha-3 precursor	Raft	7	40/1051	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
416	–	IPI00306604	ITGA5	Integrin alpha-5 precursor	Non-raft	3	42/1049	–	0.5	1.5	0.3	1	2	0.5	0	1	0.0
417	++++	IPI00010697	ITGA6	Isoform Alpha-6X1X2B of Integrin alpha-6 precursor	Non-raft	3	38/1130	++++	2.5	0.0	8.3	2	0	6.7	3	0	10.0
418	–	IPI00027505	ITGAV	Integrin alpha-V precursor	Non-raft	3	33/1048	–	0.5	1.5	0.3	1	2	0.5	0	1	0.0
419	–	IPI00217561	ITGB1	Isoform Beta-1C of Integrin beta-1 precursor	Raft	4	59/825	–	0.0	3.0	0.0	0	4	0.0	0	2	0.0
420	–	IPI00645194	ITGB1	integrin beta 1 isoform 1A precursor	Non-raft	25	276/798	–	19.5	34.0	0.6	22	46	0.5	17	22	0.8
421	+++++	IPI00027422	ITGB4	Isoform Beta-4C of Integrin beta-4 precursor	Non-raft	14	158/1822	+++++	8.5	0.5	17.0	10	1	10.0	7	0	23.3
422	+++	IPI00031821	ITM2B	Integral membrane protein 2B	Raft	3	48/266	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
423	+++++	IPI00016014	ITM2C	Isoform 1 of Integral membrane protein 2C	Non-raft	5	68/267	+++++	3.5	0.0	11.7	4	0	13.3	3	0	10.0
		IPI00016014	ITM2C	Isoform 1 of Integral membrane protein 2C	Raft	7	97/267	+++++	3.5	0.0	11.7	6	0	20.0	1	0	3.3
424	+	IPI00011916	JTV1	Multisynthetase complex auxiliary component p38	Non-raft	2	21/320	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
425	–	IPI00554711	JUP	Junction plakoglobin	Non-raft	13	183/745	–	6.5	8.0	0.8	7	6	1.2	6	10	0.6
		IPI00554711	JUP	Junction plakoglobin	Raft	19	265/745	–	13.0	10.5	1.2	20	14	1.4	6	7	0.9
426	–	IPI00014238	KARS	Lysyl-tRNA synthetase	Non-raft	2	27/597	–	2.5	2.0	1.3	3	2	1.5	2	2	1.0
		IPI00014238	KARS	Lysyl-tRNA synthetase	Raft	5	57/597	–	2.0	1.5	1.3	4	3	1.3	0	0	0.0
427	+++++	IPI00029046	KIAA0152	Protein KIAA0152 precursor	Non-raft	9	103/292	++	9.0	2.0	4.5	13	2	6.5	5	2	2.5
		IPI00029046	KIAA0152	Protein KIAA0152 precursor	Raft	5	57/292	+++++	7.5	0.0	25.0	8	0	26.7	7	0	23.3
428	–	IPI00004584	KIAA0391	Protein KIAA0391	Non-raft	3	30/567	–	2.0	1.5	1.3	2	2	1.0	2	1	2.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
429	+++	IPI00006130	KIAA0494	Uncharacterized calcium-binding protein KIAA0494	Non-raft	2	32/495	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
430	+	IPI00006499	KIAA0753	KIAA0753	Non-raft	2	16/967	+	1.0	0.5	2.0	2	0	6.7	0	1	0.0
431	+++	IPI00217007	KIAA2013	Novel protein	Non-raft	2	27/667	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
432	+	IPI00001639	KPNB1	Importin beta-1 subunit	Non-raft	8	95/876	–	5.5	4.5	1.2	7	4	1.8	4	5	0.8
		IPI00001639	KPNB1	Importin beta-1 subunit	Raft	4	58/876	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
433	+++++	IPI00423568	KRAS	Isoform 2A of GTPase KRas	Non-raft	7	80/189	+++++	6.5	0.0	21.7	6	0	20.0	7	0	23.3
434	–	IPI00328753	KTN1	Isoform 1 of Kinectin	Raft	13	160/1357	–	4.5	4.5	1.0	9	9	1.0	0	0	0.0
435	+	IPI00294186	LACTB	Isoform 1 of Serine beta-lactamase-like protein LACTB	Raft	4	53/547	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
436	–	IPI00641693	LAMA5	400 kDa protein	Raft	10	149/3695	–	2.0	4.0	0.5	4	8	0.5	0	0	0.0
437	–	IPI00296922	LAMB2	Laminin beta-2 chain precursor	Raft	7	88/1798	–	1.5	2.0	0.8	3	4	0.8	0	0	0.0
438	–	IPI00299404	LAMB3	Laminin beta-3 chain precursor	Non-raft	4	64/1172	–	0.5	1.5	0.3	1	3	0.3	0	0	0.0
439	–	IPI00298281	LAMC1	Laminin gamma-1 chain precursor	Non-raft	3	45/1609	–	0.0	1.5	0.0	0	3	0.0	0	0	0.0
		IPI00298281	LAMC1	Laminin gamma-1 chain precursor	Raft	6	82/1609	–	1.5	2.5	0.6	3	5	0.6	0	0	0.0
440	+++	IPI00004503	LAMP1	lysosomal-associated membrane protein 1	Non-raft	4	49/417	+++	2.5	0.5	5.0	4	1	4.0	1	0	3.3
441	+	IPI00419237	LAP3	leucine aminopeptidase 3	Non-raft	3	35/519	+	2.0	1.0	2.0	3	1	3.0	1	1	1.0
442	+++++	IPI00014172	LAPTM4A	Lysosomal-associated transmembrane protein 4A	Non-raft	4	47/233	+++++	3.5	0.0	11.7	4	0	13.3	3	0	10.0
		IPI00014172	LAPTM4A	Lysosomal-associated transmembrane protein 4A	Raft	4	55/233	+++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
443	–	IPI00395347	LARP4	c-Mpl binding protein isoform a	Raft	4	34/724	–	2.0	1.5	1.3	3	3	1.0	1	0	3.3
444	+++	IPI00103994	LARS	Leucyl-tRNA synthetase, cytoplasmic	Non-raft	3	53/1176	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
445	–	IPI00000861	LASP1	Isoform 1 of LIM and SH3 domain protein 1	Non-raft	3	39/261	–	1.0	1.5	0.7	2	3	0.7	0	0	0.0
446	–	IPI00305304	LASS2	LAG1 longevity assurance homolog 2	Non-raft	2	25/380	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
447	++	IPI00395993	LAT2	Isoform 1 of Linker for activation of T-cells family member 2	Raft	2	33/243	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
448	+	IPI00292135	LBR	Lamin-B receptor	Non-raft	2	34/615	+	2.5	1.0	2.5	3	2	1.5	2	0	6.7
449	++	IPI00394952	LCK	lymphocyte-specific protein tyrosine kinase precursor	Non-raft	2	18/536	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
450	+	IPI00217966	LDHA	lactate dehydrogenase A	Non-raft	12	162/332	+	9.5	4.5	2.1	15	8	1.9	4	1	4.0
451	–	IPI00219217	LDHB	L-lactate dehydrogenase B chain	Non-raft	6	74/334	–	3.5	4.0	0.9	5	7	0.7	2	1	2.0
452	–	IPI00000070	LDLR	Low-density lipoprotein receptor precursor	Non-raft	6	71/860	–	2.0	3.0	0.7	3	5	0.6	1	1	1.0
453	+	IPI00045839	LEPRE1	Isoform 3 of Prolyl 3-hydroxylase 1 precursor	Non-raft	2	22/804	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
454	+++++	IPI00219219	LGALS1	Galectin-1	Non-raft	6	77/135	+++++	13.0	1.5	8.7	13	1	13.0	13	2	6.5
		IPI00219219	LGALS1	Galectin-1	Raft	9	103/135	+	14.5	6.0	2.4	18	12	1.5	11	0	36.7
455	–	IPI00008918	LIMA1	Isoform Beta of LIM domain and actin-binding protein 1	Raft	11	147/759	–	6.5	5.0	1.3	11	10	1.1	2	0	6.7
456	–	IPI00009950	LMAN2	Vesicular integral-membrane protein VIP36 precursor	Non-raft	2	23/356	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
457	+++	IPI00020007	LMBRD1	LMBR1 domain containing 1	Non-raft	2	26/540	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
458	–	IPI00021405	LMNA	Isoform A of Lamin-A/C	Raft	22	275/664	–	11.5	10.5	1.1	20	17	1.2	3	4	0.8
459	+++++	IPI00221240	LNPEP	Isoform 2 of Leucyl-cystinyl aminopeptidase	Non-raft	17	184/1011	+++++	10.0	0.0	33.3	14	0	46.7	6	0	20.0
460	++++	IPI00293336	LOC153364	similar to metallo-beta-lactamase superfamily protein	Non-raft	6	73/279	++++	3.0	0.0	10.0	5	0	16.7	1	0	3.3
461	+++	IPI00373972	LOC388564	PREDICTED: hypothetical protein	Non-raft	2	20/176	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
		IPI00373972	LOC388564	PREDICTED: hypothetical protein	Raft	2	20/176	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
462	+	IPI00383071	LOC388642	RcTPI1 (Fragment)	Raft	2	23/249	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
463	+++	IPI00291695	LOC493869	CDNA FLJ23636 fis, clone CAS07176	Non-raft	3	35/209	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
464	+	IPI00738655	LOC653781	PREDICTED: similar to Prostate, ovary, testis expressed protein on chromosome 2	Raft	6	57/1038	+	10.0	5.5	1.8	4	4	1.0	16	7	2.3
465	+	IPI00171626	LPCAT1	1-acylglycerophosphocholine O-acyltransferase 1	Non-raft	6	84/534	+	4.0	2.5	1.6	6	3	2.0	2	2	1.0
466	–	IPI0002															

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
467	+++	IPI00414231	LRP10	Isoform 1 of Low-density lipoprotein receptor-related protein 10 precursor	Non-raft	2	28/713	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
		IPI00414231	LRP10	Isoform 1 of Low-density lipoprotein receptor-related protein 10 precursor	Raft	2	28/713	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
468	++	IPI00021027	LRP12	Low-density lipoprotein receptor-related protein 12 precursor	Non-raft	2	18/859	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
469	-	IPI00783271	LRPPRC	Leucine-rich PPR motif-containing protein	Non-raft	21	279/1394	-	8.0	8.5	0.9	13	12	1.1	3	5	0.6
470	+++++	IPI00427739	LRRC1	Isoform 1 of Leucine-rich repeat-containing protein 1	Non-raft	12	205/524	+++++	13.5	0.0	45.0	13	0	43.3	14	0	46.7
		IPI00427739	LRRC1	Isoform 1 of Leucine-rich repeat-containing protein 1	Raft	3	47/524	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
471	++	IPI00170935	LRRC47	Leucine-rich repeat-containing protein 47	Raft	2	30/583	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
472	+	IPI00396321	LRRC59	Leucine-rich repeat-containing protein 59	Non-raft	4	47/307	+	1.5	1.0	1.5	2	2	1.0	1	0	3.3
		IPI00396321	LRRC59	Leucine-rich repeat-containing protein 59	Raft	2	22/307	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
473	-	IPI00410324	LSM12	LSM12 homolog	Raft	2	24/195	-	0.5	1.0	0.5	1	2	0.5	0	0	0.0
474	+++++	IPI00409640	LSR	Isoform 1 of Lipolysis-stimulated lipoprotein receptor	Non-raft	9	111/649	+++++	14.5	0.5	29.0	18	1	18.0	11	0	36.7
		IPI00409640	LSR	Isoform 1 of Lipolysis-stimulated lipoprotein receptor	Raft	12	187/649	+++++	13.0	0.0	43.3	17	0	56.7	9	0	30.0
475	-	IPI00219077	LTA4H	LTA4H protein	Non-raft	2	23/611	-	0.0	1.0	0.0	0	2	0.0	0	0	0.0
476	+++++	IPI00298625	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	Non-raft	25	300/512	+++++	20.5	1.0	20.5	27	1	27.0	14	1	14.0
		IPI00298625	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	Raft	11	127/512	+++++	9.5	0.5	19.0	8	1	8.0	10	0	33.3
477	+++	IPI00007321	LYPLA1	Isoform 1 of Acyl-protein thioesterase 1	Non-raft	2	27/263	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
478	+++++	IPI00025049	M6PR	Cation-dependent mannose-6-phosphate receptor precursor	Non-raft	7	87/277	+++++	7.0	1.5	4.7	9	3	3.0	5	0	16.7
		IPI00025049	M6PR	Cation-dependent mannose-6-phosphate receptor precursor	Raft	2	32/277	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
479	+	IPI00396171	MAP4	Isoform 1 of Microtubule-associated protein 4	Non-raft	3	33/1152	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
480	+	IPI00008240	MARS	Methionyl-tRNA synthetase, cytoplasmic	Non-raft	7	73/900	+	4.0	2.0	2.0	5	4	1.3	3	0	10.0
481	+	IPI00017297	MATR3	Matrin-3	Raft	5	89/847	+	2.5	1.0	2.5	5	2	2.5	0	0	0.0
482	+++++	IPI00016334	MCAM	Isoform 1 of Cell surface glycoprotein MUC18 precursor	Non-raft	8	123/646	+++++	7.0	0.0	23.3	5	0	16.7	8	0	26.7
483	-	IPI00784044	MCCC2	Isoform 1 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial precursor	Non-raft	2	22/563	-	0.5	0.5	1.0	1	0	3.3	0	1	0.0
484	-	IPI00184330	MCM2	DNA replication licensing factor MCM2	Non-raft	4	42/904	-	1.0	1.0	1.0	2	2	1.0	0	0	0.0
		IPI00184330	MCM2	DNA replication licensing factor MCM2	Raft	3	34/904	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
485	+	IPI00299904	MCM7	Isoform 1 of DNA replication licensing factor MCM7	Non-raft	3	34/719	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
486	-	IPI00291005	MDH1	Malate dehydrogenase, cytoplasmic	Non-raft	2	26/334	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
487	-	IPI00291006	MDH2	Malate dehydrogenase, mitochondrial precursor	Non-raft	13	166/338	-	8.5	9.5	0.9	13	8	1.6	4	11	0.4
488	-	IPI00418234	MECP2	Methyl-CpG-binding protein 2	Non-raft	2	22/486	-	0.5	1.5	0.3	1	3	0.3	0	0	0.0
489	+	IPI00301139	MED17	CRSP complex subunit 6	Raft	4	47/651	+	2.0	1.0	2.0	4	2	2.0	0	0	0.0
490	+	IPI00022239	METAP1	Methionine aminopeptidase 1	Non-raft	2	22/386	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
		IPI00022239	METAP1	Methionine aminopeptidase 1	Raft	3	44/386	++	2.0	0.5	4.0	3	1	3.0	1	0	3.3
491	+++	IPI00090807	METTL7B	Methyltransferase-like protein 7B precursor	Non-raft	3	42/277	+++	2.0	0.0	6.7	3	0	10.0	1	0	3.3
492	++	IPI00002236	MFGE8	Lactadherin precursor	Raft	2	31/387	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
493	++++	IPI00395906	MGC59937	Similar to RIKEN cDNA 2310002J15 gene	Non-raft	2	40/144	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00395906	MGC59937	Similar to RIKEN cDNA 2310002J15 gene	Raft	3	59/144	++++	3.5	0.0	11.7	6	0	20.0	1	0	3.3
494	+	IPI00004233	MKI67	Isoform Long of Antigen KI-67	Raft	6	70/3256	+	2.5	1.5	1.7	5	3	1.7	0	0	0.0
495	+++++	IPI00218398	MMP14	Matrix metalloproteinase-14 precursor	Non-raft	10	88/582	+++++	5.5	0.0	18.3	7	0	23.3	4	0	13.3
496	+++	IPI00215610	MPP1	55 kDa erythrocyte membrane protein	Non-raft	3	45/466	+++	2.0	0.0	6.7	1	0	3.3	3	0	10.0
497	+++++	IPI00174976	MPP5	Isoform 1 of MAGUK p55 subfamily member 5	Non-raft	2	30/675	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
		IPI00174976	MPP5	Isoform 1 of MAGUK p55 subfamily member 5	Raft	4	63/675	+++++	3.0	0.0	10.0	3	0	10.0	3	0	10.0
498	+++++	IPI00303280	MPP6	MAGUK p55 subfamily member 6	Non-raft	11	164/540	+++++	9.5	0.0	31.7	11	0	36.7	8	0	26.7

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
499	+++++	IPI00017515	MREG	DSU protein	Non-raft	4	47/214	+++++	3.0	0.0	10.0	3	0	10.0	3	0	10.0
500	+++	IPI00219365	MSN	Moesin	Non-raft	15	173/577	+++	8.0	1.5	5.3	14	3	4.7	2	0	6.7
501	+++++	IPI00328715	MTDH	Protein LYRIC	Non-raft	6	74/582	+++++	6.5	0.0	21.7	7	0	23.3	6	0	20.0
		IPI00328715	MTDH	Protein LYRIC	Raft	4	47/582	+++++	7.0	0.0	23.3	7	0	23.3	7	0	23.3
502	–	IPI00218342	MTHFD1	C-1-tetrahydrofolate synthase, cytoplasmic	Non-raft	12	154/935	–	3.0	6.0	0.5	5	7	0.7	1	5	0.2
503	+++++	IPI00385172	MUC1	Mucin 1, transmembrane	Non-raft	5	67/241	+++++	3.5	0.0	11.7	3	0	10.0	5	0	16.7
		IPI00385172	MUC1	Mucin 1, transmembrane	Raft	6	76/241	+++++	6.0	0.0	20.0	8	0	26.7	4	0	13.3
504	+++	IPI00102685	MYADM	Myeloid-associated differentiation marker	Raft	2	33/322	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
505	–	IPI00019502	MYH9	Myosin-9	Non-raft	17	240/1960	–	6.0	8.0	0.8	11	14	0.8	1	2	0.5
		IPI00019502	MYH9	Myosin-9	Raft	2	24/1960	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
506	–	IPI00010418	MYO1C	Myosin Ic	Raft	4	56/1028	–	1.0	1.0	1.0	2	2	1.0	0	0	0.0
507	++	IPI00023748	NACA	Nascent polypeptide-associated complex subunit alpha	Raft	3	47/215	++	2.0	0.5	4.0	3	1	3.0	1	0	3.3
508	–	IPI00023860	NAP1L1	Nucleosome assembly protein 1-like 1	Non-raft	2	28/391	–	0.5	0.5	1.0	1	0	3.3	0	1	0.0
509	++	IPI00306960	NARS	Asparaginyl-tRNA synthetase, cytoplasmic	Non-raft	2	22/548	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
510	++	IPI00444262	NCL	CDNA FLJ45706 fis, clone FEBRA2028457, highly similar to Nucleolin	Non-raft	2	19/603	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
511	++	IPI00470649	NCLN	Isoform 1 of Nicalin precursor	Non-raft	6	73/563	++	3.5	1.0	3.5	6	2	3.0	1	0	3.3
512	+++++	IPI00021983	NCSTN	Isoform 1 of Nicastrin precursor	Non-raft	5	83/709	+++++	4.0	1.0	4.0	3	0	10.0	5	2	2.5
		IPI00021983	NCSTN	Isoform 1 of Nicastrin precursor	Raft	2	20/709	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
513	+++	IPI00012235	NDFIP1	Isoform 1 of NEDD4 family-interacting protein 1	Non-raft	2	28/221	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00012235	NDFIP1	Isoform 1 of NEDD4 family-interacting protein 1	Raft	3	28/221	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
514	–	IPI00604664	NDUFS1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	Non-raft	6	86/741	–	2.5	2.5	1.0	5	3	1.7	0	2	0.0
515	–	IPI00010346	NLN	Neurolysin, mitochondrial precursor	Non-raft	2	21/704	–	1.0	1.0	1.0	1	1	1.0	1	1	1.0
516	+++	IPI00012048	NME1	Nucleoside diphosphate kinase A	Non-raft	2	21/152	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
517	–	IPI00218830	NMT1	Isoform Short of Glycylpeptide N-tetradecanoyltransferase 1	Non-raft	3	41/416	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
518	–	IPI00329352	NOMO1	Nodal modulator 1 precursor	Non-raft	4	49/1222	–	1.0	1.5	0.7	2	3	0.7	0	0	0.0
519	+++	IPI00304596	NONO	Non-POU domain-containing octamer-binding protein	Non-raft	3	43/471	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
		IPI00304596	NONO	Non-POU domain-containing octamer-binding protein	Raft	8	89/471	+	4.5	1.5	3.0	9	3	3.0	0	0	0.0
520	++	IPI00017672	NP	CDNA FLJ25678 fis, clone TST04067, highly similar to PURINE NUCLEOSIDE PHOSPHORYLASE	Non-raft	2	31/293	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
521	+++++	IPI00005107	NPC1	Niemann-Pick C1 protein precursor	Non-raft	17	260/1278	+++++	18.5	5.5	3.4	21	5	4.2	16	6	2.7
522	++	IPI00026216	NPEPPS	Puromycin-sensitive aminopeptidase	Non-raft	2	25/919	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
523	+	IPI00001676	NPLOC4	Isoform 2 of Nuclear protein localization protein 4 homolog	Non-raft	7	94/617	+	4.0	2.5	1.6	7	3	2.3	1	2	0.5
524	++	IPI00220740	NPM1	Isoform 2 of Nucleophosmin	Non-raft	2	36/265	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
		IPI00220740	NPM1	Isoform 2 of Nucleophosmin	Raft	7	88/265	+	10.0	4.0	2.5	13	8	1.6	7	0	23.3
525	++++	IPI00012069	NQO1	NAD(P)H dehydrogenase [quinone] 1	Non-raft	5	60/274	++++	3.5	0.5	7.0	5	1	5.0	2	0	6.7
526	+++++	IPI00000005	NRAS	GTPase NRas precursor	Non-raft	12	123/189	+++++	14.5	0.5	29.0	14	0	46.7	15	1	15.0
		IPI00000005	NRAS	GTPase NRas precursor	Raft	2	21/189	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
527	+++++	IPI00299594	NRP1	Isoform 1 of Neuropilin-1 precursor	Non-raft	7	114/923	+++++	6.0	0.0	20.0	4	0	13.3	8	0	26.7
		IPI00299594	NRP1	Isoform 1 of Neuropilin-1 precursor	Raft	10	188/923	+++++	6.5	0.0	21.7	9	0	30.0	4	0	13.3
528	+++++	IPI00017231	NRSN2	Protein C20orf98	Non-raft	7	94/204	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
529	–	IPI00006451	NSF	Vesicle-fusing ATPase	Non-raft	3	35/744	–	1.0	1.5	0.7	1	3	0.3	1	0	3.3
530	+	IPI00306369	NSUN2	NOL1/NOP2/Sun domain family 2 protein	Non-raft	6	71/767	+	3.0	2.0	1.5	4	3	1.3	2	1	2.0
531	+	IPI00009456	NT5E	5'-nucleotidase precursor	Non-raft	4	81/574	+	2.0	1.0	2.0	2	2	1.0	2	0	6.7

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
		IPI00009456	NT5E	5'-nucleotidase precursor	Raft	8	121/574	+	6.5	2.5	2.6	8	3	2.7	5	2	2.5
532	+	IPI00171664	NUP43	Nucleoporin 43kDa	Raft	2	23/441	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
533	–	IPI00022334	OAT	Ornithine aminotransferase, mitochondrial precursor	Non-raft	5	82/439	–	2.0	1.5	1.3	4	3	1.3	0	0	0.0
534	+	IPI00098902	OGDH	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide) isoform 1 precursor	Non-raft	3	36/1023	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
535	+++++	IPI00022674	OSMR	oncostatin M receptor	Non-raft	9	128/979	+++++	6.5	0.5	13.0	6	0	20.0	7	1	7.0
		IPI00022674	OSMR	oncostatin M receptor	Raft	4	61/979	+++	2.0	0.0	6.7	3	0	10.0	1	0	3.3
536	+	IPI00026516	OXCT1	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor	Non-raft	2	32/520	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
537	+	IPI00010796	P4HB	Protein disulfide-isomerase precursor	Non-raft	19	241/508	+	16.5	8.0	2.1	22	9	2.4	11	7	1.6
538	–	IPI00299000	PA2G4	Proliferation-associated protein 2G4	Raft	9	104/394	–	4.5	3.5	1.3	8	7	1.1	1	0	3.3
539	++	IPI00008524	PABPC1	Isoform 1 of Polyadenylate-binding protein 1	Non-raft	5	70/636	+++	3.0	0.5	6.0	2	0	6.7	4	1	4.0
		IPI00008524	PABPC1	Isoform 1 of Polyadenylate-binding protein 1	Raft	17	207/636	–	14.0	12.0	1.2	19	16	1.2	9	8	1.1
540	–	IPI00012726	PABPC4	Isoform 1 of Polyadenylate-binding protein 4	Raft	14	179/644	–	9.0	8.0	1.1	11	10	1.1	7	6	1.2
541	+++++	IPI00329572	PACSIN3	49 kDa protein	Non-raft	5	67/424	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
		IPI00329572	PACSIN3	49 kDa protein	Raft	10	122/424	+++++	9.5	0.0	31.7	11	0	36.7	8	0	26.7
542	+++	IPI00020464	PAG1	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1	Raft	3	60/432	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
543	–	IPI00217223	PAICS	Multifunctional protein ADE2	Non-raft	4	49/451	–	2.0	2.0	1.0	3	3	1.0	0	2	0.0
544	++++	IPI00301023	PALM	Isoform 1 of Paralemmmin	Non-raft	4	43/387	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
		IPI00301023	PALM	Isoform 1 of Paralemmmin	Raft	3	33/387	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
545	+++	IPI00073769	PALM2	A kinase	Non-raft	3	34/433	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
		IPI00073769	PALM2	A kinase	Raft	4	49/433	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
546	+	IPI00449049	PARP1	Poly [ADP-ribose] polymerase 1	Raft	4	56/1014	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
547	++	IPI00018873	PBEF1	Isoform 1 of Nicotinamide phosphoribosyltransferase	Non-raft	2	35/491	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
548	–	IPI00016610	PCBP1	Poly(rC)-binding protein 1	Non-raft	6	88/356	–	1.5	3.5	0.4	3	6	0.5	0	1	0.0
		IPI00016610	PCBP1	Poly(rC)-binding protein 1	Raft	10	152/356	+	6.5	4.0	1.6	10	7	1.4	3	1	3.0
549	–	IPI00012066	PCBP2	poly(rC)-binding protein 2 isoform b	Non-raft	4	55/362	–	1.5	1.5	1.0	3	3	1.0	0	0	0.0
550	+	IPI00021700	PCNA	Proliferating cell nuclear antigen	Non-raft	2	21/261	+	1.0	0.5	2.0	2	0	6.7	0	1	0.0
551	++++	IPI00869136	PCNXL3	Isoform 1 of Pecanex-like protein 3	Raft	4	47/2034	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
552	+++	IPI00306301	PDHA1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor	Non-raft	3	28/428	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
553	–	IPI00025252	PDIA3	Protein disulfide-isomerase A3 precursor	Non-raft	21	197/505	–	15.0	14.0	1.1	19	20	1.0	11	8	1.4
		IPI00025252	PDIA3	Protein disulfide-isomerase A3 precursor	Raft	6	72/505	+	2.5	1.0	2.5	5	2	2.5	0	0	0.0
554	+	IPI00009904	PDIA4	Protein disulfide-isomerase A4 precursor	Non-raft	9	109/645	+	4.0	2.5	1.6	7	4	1.8	1	1	1.0
555	–	IPI00299571	PDIA6	CDNA FLJ45525 fis, clone BRTHA2026311, highly similar to Protein disulfide isomerase A6	Non-raft	11	153/492	–	10.0	8.5	1.2	14	11	1.3	6	6	1.0
		IPI00299571	PDIA6	CDNA FLJ45525 fis, clone BRTHA2026311, highly similar to Protein disulfide isomerase A6	Raft	4	67/492	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
556	+	IPI00023122	PDLIM7	Isoform 1 of PDZ and LIM domain protein 7	Non-raft	2	24/457	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
557	+++	IPI00293189	PERP	Isoform 1 of p53 apoptosis effector related to PMP-22	Raft	2	24/193	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
558	–	IPI00004534	PFAS	Phosphoribosylformylglycinamidine synthase	Non-raft	2	29/1338	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
559	–	IPI00009790	PFKP	6-phosphofructokinase type C	Non-raft	7	82/784	–	2.0	2.0	1.0	4	4	1.0	0	0	0.0
560	–	IPI00216691	PFN1	Profilin-1	Non-raft	5	65/140	–	3.0	3.0	1.0	3	5	0.6	3	1	3.0
561	+++	IPI00549725	PGAM1	Phosphoglycerate mutase 1	Non-raft	4	48/254	+++	2.5	0.5	5.0	4	1	4.0	1	0	3.3

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
562	–	IPI00219525	PGD	6-phosphogluconate dehydrogenase, decarboxylating	Non-raft	3	42/483	–	0.5	1.0	0.5	1	1	1.0	0	1	0.0
563	–	IPI00169383	PGK1	Phosphoglycerate kinase 1	Non-raft	4	56/417	–	3.0	2.5	1.2	6	5	1.2	0	0	0.0
564	+++	IPI00017334	PHB	Prohibitin	Non-raft	4	46/272	+++	2.5	0.5	5.0	4	1	4.0	1	0	3.3
565	–	IPI00011200	PHGDH	D-3-phosphoglycerate dehydrogenase	Non-raft	7	94/533	–	2.5	2.0	1.3	5	2	2.5	0	2	0.0
566	+++++	IPI00020124	PI4K2A	Phosphatidylinositol 4-kinase type II	Non-raft	25	333/479	+++++	23.0	0.5	46.0	31	0	103.3	15	1	15.0
		IPI00020124	PI4K2A	Phosphatidylinositol 4-kinase type II	Raft	4	36/479	+++	2.0	0.0	6.7	3	0	10.0	1	0	3.3
567	+++++	IPI00291068	PI4K2B	Phosphatidylinositol 4-kinase type-II beta	Non-raft	5	57/481	+++++	3.5	0.0	11.7	4	0	13.3	3	0	10.0
568	–	IPI00022543	PIGK	GPI-anchor transamidase precursor	Non-raft	2	23/395	–	0.0	1.0	0.0	0	2	0.0	0	0	0.0
569	+	IPI00479186	PKM2	pyruvate kinase 3 isoform 1	Non-raft	31	371/605	+	45.5	25.5	1.8	56	36	1.6	35	15	2.3
570	++	IPI00021076	PKP4	Isoform Long of Plakophilin-4	Non-raft	2	20/1211	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
571	–	IPI00010400	PLCB3	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3	Raft	2	12/1234	–	0.0	1.0	0.0	0	2	0.0	0	0	0.0
572	+++	IPI00152701	PLCD3	phospholipase C delta 3	Non-raft	3	52/789	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
573	++	IPI00012865	PLD1	Isoform PLD1A of Phospholipase D1	Raft	2	29/1074	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
574	–	IPI00337495	PLOD2	Isoform 2 of Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 precursor	Non-raft	9	135/758	–	3.0	3.5	0.9	3	5	0.6	2	2	1.0
575	–	IPI00030255	PLOD3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor	Non-raft	2	23/738	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
		IPI00030255	PLOD3	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor	Raft	3	42/738	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
576	+++	IPI00030362	PLP2	Proteolipid protein 2	Non-raft	2	28/152	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
577	–	IPI00216694	PLS3	plastin 3	Non-raft	7	82/630	–	3.5	3.5	1.0	6	3	2.0	1	3	0.3
578	+++++	IPI00005181	PLSCR1	Phospholipid scramblase 1	Non-raft	6	70/318	+++++	10.0	0.5	20.0	12	0	40.0	8	1	8.0
		IPI00005181	PLSCR1	Phospholipid scramblase 1	Raft	4	60/318	+++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
579	+++++	IPI00216127	PLSCR3	Phospholipid scramblase 3	Non-raft	4	54/295	+++++	5.5	0.0	18.3	7	0	23.3	4	0	13.3
580	+	IPI00398435	PLXNB2	PLEXIN-B2	Non-raft	16	243/1266	+	7.0	3.0	2.3	10	6	1.7	4	0	13.3
581	++	IPI00165506	POLDIP2	Polymerase delta-interacting protein 2	Non-raft	2	28/368	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
582	–	IPI00031960	POLR1A	polymerase (RNA) I polypeptide A, 194kDa	Raft	2	34/1720	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
583	+	IPI00470467	POR	NADPH--cytochrome P450 reductase	Non-raft	6	95/677	+	3.0	1.5	2.0	3	1	3.0	3	2	1.5
584	+	IPI00015018	PPA1	Inorganic pyrophosphatase	Non-raft	2	38/289	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
585	+++++	IPI00419585	PPIA	Peptidyl-prolyl cis-trans isomerase A	Non-raft	9	135/165	+++++	8.5	2.0	4.3	9	3	3.0	8	1	8.0
		IPI00419585	PPIA	Peptidyl-prolyl cis-trans isomerase A	Raft	8	122/165	+	4.5	1.5	3.0	7	3	2.3	2	0	6.7
586	–	IPI00646304	PPIB	peptidylprolyl isomerase B precursor	Non-raft	3	35/216	–	1.5	1.5	1.0	1	2	0.5	2	1	2.0
		IPI00646304	PPIB	peptidylprolyl isomerase B precursor	Raft	2	27/216	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
587	+	IPI00550451	PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	Non-raft	9	115/330	+	4.0	2.5	1.6	5	4	1.3	3	1	3.0
		IPI00550451	PPP1CA	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	Raft	11	130/330	+	5.5	2.5	2.2	7	4	1.8	4	1	4.0
588	+	IPI00218236	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	Non-raft	7	99/327	+	2.5	1.5	1.7	5	3	1.7	0	0	0.0
		IPI00218236	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	Raft	7	93/327	+	2.5	1.5	1.7	5	3	1.7	0	0	0.0
589	++	IPI00005705	PPP1CC	Isoform Gamma-1 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	Non-raft	7	103/323	+	3.0	2.0	1.5	4	3	1.3	2	1	2.0
		IPI00005705	PPP1CC	Isoform Gamma-1 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	Raft	8	100/323	++	5.0	1.5	3.3	5	3	1.7	5	0	16.7
590	++	IPI00063273	PPP1R16A	Protein phosphatase 1 regulatory subunit 16A	Non-raft	2	27/528	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
591	–	IPI00008380	PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	Non-raft	2	19/309	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
		IPI00008380	PPP2CA	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	Raft	3	51/309	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
592	+	IPI00419307	PPP2R1A	alpha isoform of regulatory subunit A, protein phosphatase 2	Non-raft	5	63/589	+	2.0	1.0	2.0	2	1	2.0	2	1	2.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
593	++	IPI00026994	PRAF2	PRA1 family protein 2	Non-raft	2	29/178	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
594	+	IPI00000874	PRDX1	Peroxiredoxin-1	Non-raft	7	66/199	+	3.0	1.5	2.0	3	1	3.0	3	2	1.5
		IPI00000874	PRDX1	Peroxiredoxin-1	Raft	8	98/199	++	6.5	2.0	3.3	8	4	2.0	5	0	16.7
595	+	IPI00027350	PRDX2	Peroxiredoxin-2	Non-raft	3	36/198	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
		IPI00027350	PRDX2	Peroxiredoxin-2	Raft	2	24/198	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
596	–	IPI00024919	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	Non-raft	3	37/256	–	2.5	2.5	1.0	2	3	0.7	3	2	1.5
		IPI00024919	PRDX3	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	Raft	3	25/256	+	1.5	1.0	1.5	2	2	1.0	1	0	3.3
597	+	IPI00011937	PRDX4	Peroxiredoxin-4	Non-raft	2	23/271	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
598	+	IPI00385449	PRKCA	Protein kinase C alpha type	Non-raft	3	35/672	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
599	–	IPI00026154	PRKCSH	Glucosidase 2 subunit beta precursor	Non-raft	9	88/535	–	4.5	7.0	0.6	6	10	0.6	3	4	0.8
600	–	IPI00296337	PRKDC	Isoform 1 of DNA-dependent protein kinase catalytic subunit	Non-raft	8	108/4128	–	0.5	4.0	0.1	1	8	0.1	0	0	0.0
601	++++	IPI00009276	PROCR	Endothelial protein C receptor precursor	Non-raft	6	71/275	++++	4.5	0.0	15.0	8	0	26.7	1	0	3.3
		IPI00009276	PROCR	Endothelial protein C receptor precursor	Raft	2	30/275	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
602	–	IPI00294004	PROS1	Vitamin K-dependent protein S precursor	Non-raft	2	19/676	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
603	++	IPI00004968	PRPF19	Pre-mRNA-processing factor 19	Non-raft	4	57/504	++	2.0	0.5	4.0	3	1	3.0	1	0	3.3
		IPI00004968	PRPF19	Pre-mRNA-processing factor 19	Raft	9	174/504	+	4.5	1.5	3.0	6	2	3.0	3	1	3.0
604	–	IPI00150269	PRPF4	Isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp4	Non-raft	2	23/522	+	1.0	0.5	2.0	1	0	3.3	1	1	1.0
		IPI00150269	PRPF4	Isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp4	Raft	3	39/522	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
605	+++++	IPI00028077	PSEN1	Isoform 1 of Presenilin-1	Non-raft	5	63/467	+++++	6.0	0.0	20.0	8	0	26.7	4	0	13.3
		IPI00028077	PSEN1	Isoform 1 of Presenilin-1	Raft	2	35/467	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
606	–	IPI00171199	PSMA3	proteasome alpha 3 subunit isoform 2	Non-raft	2	21/248	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
607	+	IPI00029623	PSMA6	Proteasome subunit alpha type 6	Non-raft	2	24/246	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
608	–	IPI00375704	PSMB5	Hypothetical protein DKFZp686I0180 (Fragment)	Non-raft	3	35/263	–	1.0	1.0	1.0	1	2	0.5	1	0	3.3
609	–	IPI00012268	PSMD2	26S proteasome non-ATPase regulatory subunit 2	Non-raft	2	29/908	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
610	++	IPI00030770	PSMG1	Isoform 1 of Down syndrome critical region protein 2	Non-raft	2	14/288	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
611	+++	IPI00103525	PSPC1	paraspeckle protein 1 isoform alpha	Raft	3	47/523	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
612	+++++	IPI00179964	PTBP1	Isoform 1 of Polypyrimidine tract-binding protein 1	Non-raft	7	99/531	+++++	4.5	0.5	9.0	5	0	16.7	4	1	4.0
		IPI00179964	PTBP1	Isoform 1 of Polypyrimidine tract-binding protein 1	Raft	11	197/531	+	6.0	4.0	1.5	7	6	1.2	5	1	5.0
613	+++++	IPI00022048	PTGFRN	Prostaglandin F2 receptor negative regulator precursor	Non-raft	15	201/879	+++++	10.0	0.0	33.3	14	0	46.7	6	0	20.0
		IPI00022048	PTGFRN	Prostaglandin F2 receptor negative regulator precursor	Raft	3	31/879	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
614	+++++	IPI00168812	PTK7	PTK7 protein tyrosine kinase 7 isoform d precursor	Non-raft	8	124/1014	+++++	5.5	0.0	18.3	8	0	26.7	3	0	10.0
615	+	IPI00008998	PTPLAD1	HSPC121	Non-raft	4	51/362	+	2.0	1.0	2.0	3	2	1.5	1	0	3.3
616	–	IPI00297261	PTPN1	Tyrosine-protein phosphatase non-receptor type 1	Non-raft	3	35/435	–	3.5	3.5	1.0	4	5	0.8	3	2	1.5
617	++	IPI00298347	PTPN11	Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11	Non-raft	2	23/593	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
618	++++	IPI00107831	PTPRF	Receptor-type tyrosine-protein phosphatase F precursor	Non-raft	7	104/1897	++++	3.5	0.5	7.0	7	1	7.0	0	0	0.0
619	+++	IPI00011651	PTPRG	Receptor-type tyrosine-protein phosphatase gamma precursor	Non-raft	3	50/1445	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
620	+++++	IPI00032903	PTRH2	Peptidyl-tRNA hydrolase 2, mitochondrial precursor	Non-raft	7	100/179	+++++	5.0	0.0	16.7	5	0	16.7	5	0	16.7
621	++++	IPI00023974	PTTG1IP	Pituitary tumor-transforming gene 1 protein-interacting protein precursor	Non-raft	3	41/180	++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
		IPI00023974	PTTG1IP	Pituitary tumor-transforming gene 1 protein-interacting protein precursor	Raft	2	30/180	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
622	+	IPI00023591	PURA	Transcriptional activator protein Pur-alpha	Raft	2	35/322	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
623	+++++	IPI00219425	PVR	Isoform Beta of Poliovirus receptor precursor	Non-raft	9	86/372	+++++	19.0	1.5	12.7	17	3	5.7	21	0	70.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
		IPI00219425	PVR	Isoform Beta of Poliovirus receptor precursor	Raft	2	25/372	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
624	+++++	IPI00022661	PVRL2	Isoform Delta of Poliovirus receptor-related protein 2 precursor	Non-raft	7	92/538	+++++	5.0	0.0	16.7	7	0	23.3	3	0	10.0
625	+	IPI00026665	QARS	GlutaminyI-tRNA synthetase	Non-raft	2	20/793	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
		IPI00026665	QARS	GlutaminyI-tRNA synthetase	Raft	3	29/793	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
626	+++++	IPI00016513	RAB10	Ras-related protein Rab-10	Non-raft	6	48/200	+++++	10.0	3.0	3.3	9	3	3.0	11	3	3.7
627	+	IPI00016373	RAB13	Ras-related protein Rab-13	Non-raft	8	90/203	+	7.5	3.0	2.5	11	5	2.2	4	1	4.0
628	+++++	IPI00291928	RAB14	Ras-related protein Rab-14	Non-raft	8	97/215	+++++	7.5	1.5	5.0	9	2	4.5	6	1	6.0
629	+++++	IPI00005719	RAB1A	RAB1A, member RAS oncogene family	Non-raft	11	111/205	+++++	11.0	1.5	7.3	13	1	13.0	9	2	4.5
630	+++++	IPI00008964	RAB1B	Ras-related protein Rab-1B	Non-raft	10	121/201	+++++	11.5	3.0	3.8	12	3	4.0	11	3	3.7
631	+	IPI00007755	RAB21	Ras-related protein Rab-21	Non-raft	7	88/225	+	4.0	1.5	2.7	7	3	2.3	1	0	3.3
632	+	IPI00031169	RAB2A	Ras-related protein Rab-2A	Non-raft	5	57/212	+	3.5	2.0	1.8	4	2	2.0	3	2	1.5
633	+	IPI00102896	RAB2B	Ras-related protein Rab-2B	Non-raft	3	41/216	+	1.5	0.5	3.0	0	0	0.0	3	1	3.0
634	+	IPI00328180	RAB34	Isoform 1 of Ras-related protein Rab-34	Non-raft	2	25/259	+	1.5	1.0	1.5	3	2	1.5	0	0	0.0
635	+++++	IPI00300096	RAB35	Ras-related protein Rab-35	Non-raft	6	67/201	+++++	6.0	1.0	6.0	8	1	8.0	4	1	4.0
636	+++	IPI00023504	RAB3A	Ras-related protein Rab-3A	Non-raft	3	19/220	+++	2.5	0.5	5.0	2	0	6.7	3	1	3.0
637	+++	IPI00300562	RAB3B	Ras-related protein Rab-3B	Non-raft	4	62/219	+++	2.5	0.5	5.0	5	1	5.0	0	0	0.0
638	+++	IPI00032808	RAB3D	Ras-related protein Rab-3D	Non-raft	5	51/219	+++	3.0	0.5	6.0	6	1	6.0	0	0	0.0
639	+	IPI00448725	RAB4B	RAB4B protein	Non-raft	2	24/121	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
640	+++++	IPI00016339	RAB5C	Ras-related protein Rab-5C	Non-raft	3	40/216	+++++	3.5	0.0	11.7	4	0	13.3	3	0	10.0
641	+	IPI00023526	RAB6A	RAB6A, member RAS oncogene family isoform b	Non-raft	2	23/208	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
642	++	IPI00016891	RAB6B	Ras-related protein Rab-6B	Non-raft	2	22/208	++	2.0	0.5	4.0	0	0	0.0	4	1	4.0
643	+	IPI00016342	RAB7A	Ras-related protein Rab-7	Non-raft	5	78/207	+	3.5	1.5	2.3	4	2	2.0	3	1	3.0
644	+++++	IPI00028481	RAB8A	Ras-related protein Rab-8A	Non-raft	7	73/207	+++++	8.0	2.0	4.0	9	2	4.5	7	2	3.5
645	++	IPI00010271	RAC1	Isoform A of Ras-related C3 botulinum toxin substrate 1 precursor	Non-raft	4	46/192	++++	4.0	0.5	8.0	2	1	2.0	6	0	20.0
		IPI00010271	RAC1	Isoform A of Ras-related C3 botulinum toxin substrate 1 precursor	Raft	5	29/192	–	3.0	2.5	1.2	6	5	1.2	0	0	0.0
646	–	IPI00019733	RAE1	mRNA-associated protein mrnp 41	Raft	3	42/368	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
647	+++++	IPI00217519	RALA	Ras-related protein Ral-A	Non-raft	7	91/206	+++++	6.0	0.0	20.0	8	0	26.7	4	0	13.3
		IPI00217519	RALA	Ras-related protein Ral-A	Raft	3	41/206	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
648	+++++	IPI00004397	RALB	Ras-related protein Ral-B	Non-raft	6	76/228	+++++	5.5	0.0	18.3	8	0	26.7	3	0	10.0
		IPI00004397	RALB	Ras-related protein Ral-B	Raft	3	28/228	+++++	3.0	0.0	10.0	3	0	10.0	3	0	10.0
649	++++	IPI00643041	RAN	GTP-binding nuclear protein Ran	Non-raft	4	49/216	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
650	–	IPI00329200	RANBP5	127 kDa protein	Non-raft	5	75/1115	–	1.5	1.5	1.0	2	3	0.7	1	0	3.3
651	+	IPI00015148	RAP1B	Ras-related protein Rap-1b precursor	Non-raft	6	62/184	+	6.0	2.0	3.0	7	3	2.3	5	1	5.0
652	+++++	IPI00019346	RAP2A	Ras-related protein Rap-2a	Non-raft	8	109/183	+++++	6.5	0.0	21.7	4	0	13.3	9	0	30.0
653	+++++	IPI00018364	RAP2B	Ras-related protein Rap-2b precursor	Non-raft	11	120/183	+++++	10.5	0.0	35.0	9	0	30.0	12	0	40.0
		IPI00018364	RAP2B	Ras-related protein Rap-2b precursor	Raft	3	42/183	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
654	+++++	IPI00009607	RAP2C	Ras-related protein Rap-2c precursor	Non-raft	11	127/183	+++++	12.5	0.5	25.0	11	1	11.0	14	0	46.7
655	–	IPI00004860	RARS	Isoform Complexed of ArginyI-tRNA synthetase, cytoplasmic	Non-raft	6	66/660	–	2.5	3.0	0.8	2	4	0.5	3	2	1.5
656	+++	IPI00031755	RCE1	CAAX prenyl protease 2	Non-raft	2	27/329	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
657	+	IPI00339384	RDH11	Isoform 1 of Retinol dehydrogenase 11	Non-raft	3	39/318	+	1.5	1.0	1.5	2	0	6.7	1	2	0.5
658	+	IPI00177940	RDH14	Retinol dehydrogenase 14	Non-raft	2	31/336	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
659	+	IPI00178431	RECQL	ATP-dependent DNA helicase Q1	Non-raft	6	81/649	+	2.5	1.5	1.7	5	3	1.7	0	0	0.0
660	++++	IPI00024670	REEP5	Receptor expression-enhancing protein 5	Non-raft	4	43/189	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
661	++++	IPI00216890	RELL1	Similar to expressed sequence AA536743	Non-raft	3	57/271	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
		IPI00216890	RELL1	Similar to expressed sequence AA536743	Raft	4	50/271	++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
662	—	IPI00017381	RFC4	Replication factor C subunit 4	Raft	6	82/363	—	2.5	3.0	0.8	3	4	0.8	2	2	1.0
663	++++	IPI00103867	RFFL	Isoform 1 of Riffifylin	Non-raft	3	58/363	++++	2.5	0.0	8.3	3	0	10.0	2	0	6.7
664	++	IPI00005250	RGS17	Regulator of G-protein signaling 17	Raft	2	16/210	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
665	++	IPI00028108	RGS19	Regulator of G-protein signaling 19	Raft	2	27/217	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
666	++++	IPI00008802	RGS20	Isoform 6 of Regulator of G-protein signaling 20	Raft	6	116/388	++++	5.5	0.0	18.3	9	0	30.0	2	0	6.7
667	++++	IPI00027500	RHOA	Transforming protein RhoA precursor	Non-raft	3	44/193	++++	3.5	0.5	7.0	2	1	2.0	5	0	16.7
668	+++++	IPI00000041	RHOB	Rho-related GTP-binding protein RhoB precursor	Non-raft	4	55/196	+++++	5.5	0.5	11.0	4	1	4.0	7	0	23.3
669	+++	IPI00027434	RHOC	Rho-related GTP-binding protein RhoC precursor	Non-raft	3	44/193	+++	2.5	0.5	5.0	2	1	2.0	3	0	10.0
670	+++++	IPI00017342	RHOG	Rho-related GTP-binding protein RhoG precursor	Non-raft	5	89/191	+++++	4.5	1.0	4.5	3	1	3.0	6	1	6.0
671	+++	IPI00023511	RNF167	RING finger protein 167 precursor	Non-raft	2	22/350	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
672	—	IPI00550069	RNH1	Ribonuclease inhibitor	Non-raft	2	26/461	—	0.5	1.5	0.3	1	2	0.5	0	1	0.0
673	+++	IPI00010405	ROR1	Isoform Long of Tyrosine-protein kinase transmembrane receptor ROR1 precursor	Non-raft	4	49/937	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
674	—	IPI00301202	RP11-217H1.1	Implantation-associated protein precursor	Non-raft	2	19/367	—	0.5	0.5	1.0	1	1	1.0	0	0	0.0
675	+++	IPI00026627	RP2	Protein XRP2	Non-raft	2	24/350	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00026627	RP2	Protein XRP2	Raft	3	33/350	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
676	++	IPI00020127	RPA1	Replication protein A 70 kDa DNA-binding subunit	Raft	9	129/616	++	5.5	1.5	3.7	9	3	3.0	2	0	6.7
677	+++	IPI00412579	RPL10A	60S ribosomal protein L10a	Raft	4	57/217	+++	2.5	0.5	5.0	4	1	4.0	1	0	3.3
678	—	IPI00376798	RPL11	ribosomal protein L11	Non-raft	5	59/178	—	2.5	2.0	1.3	2	3	0.7	3	1	3.0
		IPI00376798	RPL11	ribosomal protein L11	Raft	3	35/178	+	2.5	1.0	2.5	3	1	3.0	2	1	2.0
679	+++++	IPI00024933	RPL12	60S ribosomal protein L12	Non-raft	4	55/165	+++++	4.5	1.0	4.5	4	1	4.0	5	1	5.0
		IPI00024933	RPL12	60S ribosomal protein L12	Raft	5	63/165	+	4.5	1.5	3.0	5	2	2.5	4	1	4.0
680	+++	IPI00304612	RPL13A	60S ribosomal protein L13a	Non-raft	3	37/203	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
681	++	IPI00375511	RPL15	26 kDa protein	Non-raft	2	23/204	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
682	+++	IPI00215719	RPL18	60S ribosomal protein L18	Non-raft	2	24/188	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
683	+	IPI00219153	RPL22	60S ribosomal protein L22	Non-raft	5	60/128	+	4.0	2.0	2.0	5	4	1.3	3	0	10.0
684	++	IPI00182533	RPL28	60S ribosomal protein L28	Non-raft	2	23/137	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
685	+++++	IPI00550021	RPL3	60S ribosomal protein L3	Non-raft	4	58/403	+++++	4.5	0.5	9.0	5	1	5.0	4	0	13.3
		IPI00550021	RPL3	60S ribosomal protein L3	Raft	4	65/403	+++++	3.0	0.0	10.0	5	0	16.7	1	0	3.3
686	+++	IPI00219156	RPL30	60S ribosomal protein L30	Non-raft	3	40/115	+++	3.0	0.5	6.0	1	1	1.0	5	0	16.7
		IPI00219156	RPL30	60S ribosomal protein L30	Raft	3	40/115	+++	1.5	0.0	5.0	0	0	0.0	3	0	10.0
687	++	IPI00029731	RPL35A	60S ribosomal protein L35a	Non-raft	2	20/110	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
688	++	IPI00000494	RPL5	60S ribosomal protein L5	Non-raft	2	31/297	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
		IPI00000494	RPL5	60S ribosomal protein L5	Raft	16	171/297	+	18.5	6.5	2.8	30	13	2.3	7	0	23.3
689	+	IPI00030179	RPL7	60S ribosomal protein L7	Non-raft	2	25/248	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
690	+++	IPI00012772	RPL8	60S ribosomal protein L8	Non-raft	3	35/257	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
691	++	IPI00031691	RPL9	60S ribosomal protein L9	Non-raft	4	39/192	+	2.0	1.0	2.0	1	2	0.5	3	0	10.0
		IPI00031691	RPL9	60S ribosomal protein L9	Raft	2	41/192	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
692	+	IPI00008530	RPLP0	60S acidic ribosomal protein P0	Non-raft	4	60/317	+	3.0	1.5	2.0	3	1	3.0	3	2	1.5
		IPI00008530	RPLP0	60S acidic ribosomal protein P0	Raft	4	46/317	—	3.0	2.5	1.2	4	3	1.3	2	2	1.0
693	+	IPI00025874	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	Non-raft	12	168/646	+	10.5	6.5	1.6	13	8	1.6	8	5	1.6
694	++++	IPI00301271	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor	Non-raft	8	130/647	+++++	6.0	1.0	6.0	9	1	9.0	3	1	3.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
695	++++	IPI00025091	RPS11	40S ribosomal protein S11	Non-raft	3	33/158	++++	2.5	0.0	8.3	3	0	10.0	2	0	6.7
696	+	IPI00013917	RPS12	40S ribosomal protein S12	Non-raft	4	54/132	+	3.0	1.0	3.0	2	1	2.0	4	1	4.0
		IPI00013917	RPS12	40S ribosomal protein S12	Raft	6	67/132	+	8.0	3.5	2.3	9	6	1.5	7	1	7.0
697	+++	IPI00221091	RPS15A	40S ribosomal protein S15a	Non-raft	2	11/130	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00221091	RPS15A	40S ribosomal protein S15a	Raft	3	19/130	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
698	+	IPI00221092	RPS16	40S ribosomal protein S16	Raft	2	22/146	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
699	++	IPI00221093	RPS17	40S ribosomal protein S17	Raft	2	32/135	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
700	–	IPI00013485	RPS2	40S ribosomal protein S2	Non-raft	2	19/293	–	0.5	0.5	1.0	1	0	3.3	0	1	0.0
		IPI00013485	RPS2	40S ribosomal protein S2	Raft	4	45/293	+	1.5	1.0	1.5	1	2	0.5	2	0	6.7
701	++	IPI00012493	RPS20	40S ribosomal protein S20	Non-raft	2	19/119	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
		IPI00012493	RPS20	40S ribosomal protein S20	Raft	3	30/119	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
702	+	IPI00017448	RPS21	40S ribosomal protein S21	Raft	5	37/83	+	3.5	2.0	1.8	5	4	1.3	2	0	6.7
703	–	IPI00029750	RPS24	Isoform 1 of 40S ribosomal protein S24	Non-raft	2	27/133	–	0.5	0.5	1.0	0	1	0.0	1	0	3.3
704	+++++	IPI00179330	RPS27A	ubiquitin and ribosomal protein S27a precursor	Non-raft	6	83/156	+	11.0	3.5	3.1	17	3	5.7	5	3	1.7
		IPI00179330	RPS27A	ubiquitin and ribosomal protein S27a precursor	Raft	6	64/156	+++++	8.0	1.0	8.0	10	2	5.0	6	0	20.0
705	+	IPI00011253	RPS3	40S ribosomal protein S3	Non-raft	6	86/243	+	5.5	3.0	1.8	5	4	1.3	5	2	2.5
		IPI00011253	RPS3	40S ribosomal protein S3	Raft	12	170/243	+	9.5	5.0	1.9	13	7	1.9	6	3	2.0
706	++	IPI00419880	RPS3A	40S ribosomal protein S3a	Non-raft	2	23/264	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00419880	RPS3A	40S ribosomal protein S3a	Raft	4	54/264	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
707	++	IPI00008433	RPS5	40S ribosomal protein S5	Non-raft	3	38/204	++	5.0	1.5	3.3	5	0	16.7	5	3	1.7
		IPI00008433	RPS5	40S ribosomal protein S5	Raft	5	55/204	+	9.5	3.0	3.2	10	4	2.5	9	2	4.5
708	++	IPI00013415	RPS7	40S ribosomal protein S7	Non-raft	2	15/194	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
709	+	IPI00216587	RPS8	40S ribosomal protein S8	Non-raft	4	52/208	++	3.5	1.0	3.5	3	2	1.5	4	0	13.3
		IPI00216587	RPS8	40S ribosomal protein S8	Raft	4	40/208	–	3.0	2.5	1.2	4	3	1.3	2	1	2.0
710	+++	IPI00221088	RPS9	40S ribosomal protein S9	Raft	3	21/194	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
711	+	IPI00413108	RPSA	Ribosomal protein SA	Non-raft	3	175/300	+	2.5	1.5	1.7	3	1	3.0	2	2	1.0
		IPI00413108	RPSA	Ribosomal protein SA	Raft	12	46/300	+	16.0	8.0	2.0	18	8	2.3	14	6	2.3
712	++	IPI00023101	RQCD1	Homo sapiens protein involved in sexual development, complete cds	Raft	2	32/299	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
713	+++++	IPI00020418	RRAS	Ras-related protein R-Ras	Non-raft	10	98/218	+++++	12.5	0.5	25.0	15	0	50.0	10	1	10.0
		IPI00020418	RRAS	Ras-related protein R-Ras	Raft	2	33/218	+++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0
714	+++++	IPI00012512	RRAS2	Ras-related protein R-Ras2	Non-raft	14	162/204	+++++	18.0	0.0	60.0	17	0	56.7	19	0	63.3
		IPI00012512	RRAS2	Ras-related protein R-Ras2	Raft	6	76/204	+++++	7.5	0.0	25.0	9	0	30.0	6	0	20.0
715	+	IPI00215743	RRBP1	Isoform 3 of Ribosome-binding protein 1	Raft	18	240/1410	+	8.0	4.0	2.0	16	8	2.0	0	0	0.0
716	+++++	IPI00061267	RSPRY1	Ring finger and SPRY domain containing 1	Non-raft	8	126/576	+++++	8.0	0.5	16.0	10	1	10.0	6	0	20.0
		IPI00061267	RSPRY1	Ring finger and SPRY domain containing 1	Raft	7	98/576	+++++	8.5	0.0	28.3	9	0	30.0	8	0	26.7
717	++	IPI00021766	RTN4	Isoform 1 of Reticulon-4	Non-raft	2	28/1192	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
718	++	IPI00298289	RTN4	Isoform 2 of Reticulon-4	Non-raft	2	22/373	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
719	++	IPI00021187	RUVBL1	Isoform 1 of RuvB-like 1	Non-raft	3	38/456	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
		IPI00021187	RUVBL1	Isoform 1 of RuvB-like 1	Raft	8	108/456	+	6.5	4.0	1.6	9	6	1.5	4	2	2.0
720	–	IPI00009104	RUVBL2	RuvB-like 2	Raft	10	120/463	–	5.0	3.5	1.4	8	6	1.3	2	1	2.0
721	–	IPI00007047	S100A8	Protein S100-A8	Non-raft	2	22/93	–	2.0	1.5	1.3	1	1	1.0	2	2	1.0
722	+++++	IPI00005129	SCAMP1	Isoform 1 of Secretory carrier-associated membrane protein 1	Non-raft	11	134/338	+++++	21.0	0.0	70.0	28	0	93.3	14	0	46.7
		IPI00005129	SCAMP1	Isoform 1 of Secretory carrier-associated membrane protein 1	Raft	2	36/338	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
723	+++++	IPI00218850	SCAMP2	Secretory carrier-associated membrane protein 2	Non-raft	5	77/329	+++++	8.5	0.0	28.3	12	0	40.0	5	0	16.7

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
724	+++++	IPI00306382	SCAMP3	Isoform 1 of Secretory carrier-associated membrane protein 3	Non-raft	9	142/347	+++++	25.0	3.0	8.3	26	6	4.3	24	0	80.0
		IPI00306382	SCAMP3	Isoform 1 of Secretory carrier-associated membrane protein 3	Raft	4	51/347	++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
725	+++++	IPI00056310	SCAMP4	Secretory carrier-associated membrane protein 4	Non-raft	3	34/229	+++++	10.5	0.0	35.0	11	0	36.7	10	0	33.3
726	+++++	IPI00177968	SCARB1	Isoform 1 of Scavenger receptor class B member 1	Non-raft	11	131/509	+++++	11.5	1.5	7.7	13	2	6.5	10	1	10.0
		IPI00177968	SCARB1	Isoform 1 of Scavenger receptor class B member 1	Raft	2	20/509	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
727	+++++	IPI00217766	SCARB2	Lysosome membrane protein 2	Non-raft	10	125/478	+++++	13.0	0.0	43.3	18	0	60.0	8	0	26.7
728	++	IPI00329600	SCCPDH	Probable saccharopine dehydrogenase	Non-raft	2	22/429	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
729	+	IPI00165261	SCFD1	Sec1 family domain-containing protein 1	Non-raft	2	30/642	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
730	+++++	IPI00410666	SCRIB	Isoform 3 of Protein LAP4	Non-raft	15	212/1655	+++++	16.0	0.0	53.3	23	0	76.7	9	0	30.0
		IPI00410666	SCRIB	Isoform 3 of Protein LAP4	Raft	4	61/1655	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
731	+++	IPI00106642	SDF2L1	Dihydropyrimidinase-like 2	Non-raft	2	26/619	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
732	+	IPI00305166	SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	Non-raft	16	220/668	+	12.0	6.0	2.0	16	10	1.6	8	2	4.0
733	+++	IPI00006865	SEC22B	Vesicle-trafficking protein SEC22b	Non-raft	2	30/215	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
734	++	IPI00218922	SEC63	Translocation protein SEC63 homolog	Non-raft	2	22/760	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
735	+	IPI00185533	SEH1L	Isoform A of Nucleoporin SEH1-like	Raft	4	49/360	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
736	+	IPI00153055	SEPT10	Isoform 2 of Septin-10	Non-raft	3	36/503	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
737	+	IPI00019376	SEPT11	Septin-11	Non-raft	4	40/429	+	3.0	1.0	3.0	4	1	4.0	2	1	2.0
738	+	IPI00014177	SEPT2	Septin-2	Non-raft	9	134/361	+	6.0	2.5	2.4	6	3	2.0	6	2	3.0
739	++	IPI00216139	SEPT6	septin 6 isoform A	Non-raft	2	17/427	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
740	++++	IPI00033025	SEPT7	Septin-7	Non-raft	7	108/438	++++	3.5	0.5	7.0	5	1	5.0	2	0	6.7
		IPI00033025	SEPT7	Septin-7	Raft	3	35/438	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
741	+	IPI00784614	SEPT9	Isoform 1 of Septin-9	Non-raft	12	154/586	+	7.0	3.0	2.3	11	4	2.8	3	2	1.5
		IPI00784614	SEPT9	Isoform 1 of Septin-9	Raft	2	22/586	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
742	-	IPI00410693	SERBP1	Isoform 1 of Plasminogen activator inhibitor 1 RNA-binding protein	Raft	3	47/408	-	1.5	1.5	1.0	3	3	1.0	0	0	0.0
743	+++	IPI00413817	SERINC1	Serine incorporator 1	Non-raft	2	30/453	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
744	-	IPI00553177	SERPINA1	Alpha-1-antitrypsin precursor	Non-raft	2	32/418	-	2.0	2.5	0.8	0	0	0.0	4	5	0.8
745	-	IPI00033583	SERPINB12	Serpin B12	Non-raft	2	20/405	-	0.0	1.0	0.0	0	2	0.0	0	0	0.0
746	+	IPI00300371	SF3B3	Splicing factor 3B subunit 3	Raft	8	118/1217	+	4.0	1.5	2.7	7	3	2.3	1	0	3.3
747	-	IPI00010740	SFPQ	Isoform Long of Splicing factor, proline- and glutamine-rich	Raft	2	22/707	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
748	+++	IPI00166444	SFT2D3	Vesicle transport protein SFT2C	Non-raft	2	28/215	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
749	++	IPI00009368	SFXN1	Sideroflexin-1	Non-raft	3	46/322	++	2.0	0.5	4.0	3	1	3.0	1	0	3.3
750	-	IPI00002520	SHMT2	Serine hydroxymethyltransferase, mitochondrial precursor	Non-raft	14	182/504	-	8.0	6.5	1.2	11	9	1.2	5	4	1.3
751	+	IPI00647217	SKIV2L2	Superkiller viralicidic activity 2-like 2	Raft	7	89/1042	+	3.0	1.5	2.0	6	3	2.0	0	0	0.0
752	++	IPI00394753	SLC11A2	Isoform 1 of Natural resistance-associated macrophage protein 2	Non-raft	2	37/561	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
753	++++	IPI00006666	SLC16A3	Monocarboxylate transporter 4	Non-raft	4	64/465	++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
754	++++	IPI00375452	SLC19A1	Folate transporter 1	Non-raft	5	91/591	++++	4.0	0.0	13.3	6	0	20.0	2	0	6.7
755	+++++	IPI00019472	SLC1A5	Neutral amino acid transporter B(0)	Non-raft	15	211/541	+++++	20.5	1.5	13.7	25	2	12.5	16	1	16.0
756	+	IPI00022202	SLC25A3	Isoform A of Phosphate carrier protein, mitochondrial precursor	Non-raft	7	74/362	+	5.5	3.0	1.8	7	6	1.2	4	1	4.0
757	+++++	IPI00007188	SLC25A5	ADP/ATP translocase 2	Non-raft	9	89/298	+++++	8.0	2.0	4.0	9	2	4.5	7	2	3.5
758	+	IPI00291467	SLC25A6	ADP/ATP translocase 3	Non-raft	8	85/298	+	8.0	4.5	1.8	8	5	1.6	8	4	2.0
759	++++	IPI00032107	SLC26A2	Sulfate transporter	Non-raft	10	129/739	++++	5.5	0.0	18.3	9	0	30.0	2	0	6.7
		IPI00032107	SLC26A2	Sulfate transporter	Raft	4	53/739	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
760	++	IPI00024787	SLC27A2	Very-long-chain acyl-CoA synthetase	Non-raft	2	22/620	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
761	++	IPI00550382	SLC29A1	Equilibrative nucleoside transporter 1	Non-raft	2	34/535	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
762	+	IPI00220194	SLC2A1	Solute carrier family 2, facilitated glucose transporter member 1	Non-raft	6	47/492	+	6.5	3.0	2.2	7	5	1.4	6	3	2.0
		IPI00220194	SLC2A1	Solute carrier family 2, facilitated glucose transporter member 1	Raft	3	35/492	+	4.5	3.0	1.5	5	4	1.3	4	2	2.0
763	+++	IPI00179969	SLC2A6	CDNA FLJ90355 fis, clone NT2RP2003469, moderately similar to Solute carrier family 2, facilitated glucose transporter, member 6	Non-raft	3	27/445	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
764	++++	IPI00784764	SLC30A1	solute carrier family 30 (zinc transporter), member 1	Non-raft	4	71/507	++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0
765	+++++	IPI00384867	SLC35B2	Isoform 2 of Adenosine 3'-phospho 5'-phosphosulfate transporter 1	Non-raft	4	56/392	+++++	5.0	0.0	16.7	5	1	5.0	5	0	16.7
766	+++++	IPI00410034	SLC38A2	Putative 40-9-1 protein	Non-raft	5	74/506	+++++	4.5	0.5	9.0	5	1	5.0	4	0	13.3
767	++	IPI00100585	SLC39A1	Zinc transporter ZIP1	Non-raft	2	45/324	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
768	+	IPI00014236	SLC39A14	KIAA0062 protein	Non-raft	3	45/492	+	4.5	1.5	3.0	6	2	3.0	3	1	3.0
769	+	IPI00027493	SLC3A2	4F2 cell-surface antigen heavy chain	Non-raft	13	175/529	+	9.0	5.0	1.8	13	7	1.9	5	3	1.7
770	+++++	IPI00221393	SLC44A1	Isoform 1 of Choline transporter-like protein 1	Non-raft	12	151/657	+++++	19.0	0.0	63.3	23	0	76.7	15	0	50.0
771	+++	IPI00293074	SLC44A2	Isoform 2 of Choline transporter-like protein 2	Non-raft	3	34/709	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
772	+++	IPI00043883	SLC46A1	Isoform 1 of Heme carrier protein 1	Non-raft	2	25/459	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
773	+++	IPI00383597	SLC4A2	Isoform A of Anion exchange protein 2	Non-raft	3	36/1241	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
774	++++	IPI00031822	SLC5A6	Sodium-dependent multivitamin transporter	Non-raft	5	67/635	++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
775	+++++	IPI00027728	SLC7A1	High-affinity cationic amino acid transporter 1	Non-raft	4	42/629	+++++	4.0	0.0	13.3	5	0	16.7	3	0	10.0
776	+	IPI00008986	SLC7A5	Large neutral amino acids transporter small subunit 1	Non-raft	2	32/507	+	2.0	1.0	2.0	4	2	2.0	0	0	0.0
777	-	IPI00385034	SLC9A3R2	Isoform 1 of Na(+)/H(+) exchange regulatory cofactor NHE-RF2	Raft	2	22/337	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
778	++++	IPI00100858	SLCO4A1	Isoform 1 of Solute carrier organic anion transporter family member 4A1	Non-raft	4	55/722	++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0
779	+	IPI00291939	SMC1A	Structural maintenance of chromosome 1-like 1 protein	Raft	4	30/1233	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
780	+++++	IPI00010438	SNAP23	Isoform SNAP-23a of Synaptosomal-associated protein 23	Non-raft	9	130/211	+++++	9.0	0.0	30.0	9	0	30.0	9	0	30.0
		IPI00010438	SNAP23	Isoform SNAP-23a of Synaptosomal-associated protein 23	Raft	15	179/211	+++++	14.5	0.5	29.0	22	1	22.0	7	0	23.3
781	-	IPI00140420	SND1	Staphylococcal nuclease domain-containing protein 1	Non-raft	10	148/910	-	6.0	6.0	1.0	6	8	0.8	6	4	1.5
		IPI00140420	SND1	Staphylococcal nuclease domain-containing protein 1	Raft	24	322/910	+	13.0	8.0	1.6	19	14	1.4	7	2	3.5
782	+	IPI00009505	SNTB2	Isoform 1 of Beta-2-syntrophin	Non-raft	2	23/540	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
783	++	IPI00472939	SPCS2	Signal peptidase complex subunit 2	Non-raft	2	21/227	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
784	-	IPI00300299	SPCS3	Signal peptidase complex subunit 3	Non-raft	2	21/180	-	0.5	0.5	1.0	0	1	0.0	1	0	3.3
785	+++	IPI00012913	SPRY2	SPRY2 protein	Non-raft	2	28/353	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
786	+	IPI00413728	SPTAN1	Isoform 1 of Spectrin alpha chain, brain	Raft	10	132/2472	+	5.5	2.0	2.8	10	4	2.5	1	0	3.3
787	+	IPI00005745	SPTLC1	Serine palmitoyltransferase 1	Non-raft	4	55/473	+	3.0	1.0	3.0	5	1	5.0	1	1	1.0
788	+	IPI00009634	SQRDL	Sulfide:quinone oxidoreductase, mitochondrial precursor	Non-raft	2	24/450	+	2.0	1.0	2.0	2	1	2.0	2	1	2.0
789	-	IPI00179473	SQSTM1	48 kDa protein	Non-raft	4	72/440	-	4.0	3.0	1.3	6	4	1.5	2	2	1.0
		IPI00179473	SQSTM1	48 kDa protein	Raft	8	175/440	-	10.5	10.0	1.1	16	16	1.0	5	4	1.3
790	-	IPI00102936	SRP68	Isoform 2 of Signal recognition particle 68 kDa protein	Non-raft	4	67/596	-	1.5	1.5	1.0	2	2	1.0	1	1	1.0
791	-	IPI00290439	SRPK1	Isoform 1 of Serine/threonine-protein kinase SRPK1	Raft	2	18/826	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
792	+	IPI00019385	SSR4	Hypothetical protein SSR4 (Fragment)	Non-raft	3	31/184	+	2.0	1.0	2.0	3	1	3.0	1	1	1.0
793	++++	IPI00012434	STARD3NL	Isoform 1 of MLN64 N-terminal domain homolog	Non-raft	4	46/234	++++	3.5	0.0	11.7	6	0	20.0	1	0	3.3
794	++	IPI00005846	STEAP1	Six transmembrane epithelial antigen of prostate 1	Non-raft	2	21/486	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
795	-	IPI00013894	STIP1	Stress-induced-phosphoprotein 1	Non-raft	5	62/543	-	1.5	2.0	0.8	2	3	0.7	1	1	1.0
796	+++++	IPI00219682	STOM	Erythrocyte band 7 integral membrane protein	Non-raft	13	140/288	+++++	23.5	1.0	23.5	19	2	9.5	28	0	93.3
		IPI00219682	STOM	Erythrocyte band 7 integral membrane protein	Raft	15	188/288	+++++	28.0	0.0	93.3	34	0	113.3	22	0	73.3

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
797	+++	IPI00334190	STOML2	Stomatin-like protein 2	Non-raft	6	118/356	+++	3.0	0.5	6.0	6	1	6.0	0	0	0.0
798	-	IPI00294536	STRAP	Serine-threonine kinase receptor-associated protein	Non-raft	2	33/363	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
799	-	IPI00297492	STT3A	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A	Non-raft	5	57/705	-	2.0	2.0	1.0	4	3	1.3	0	1	0.0
800	++	IPI00293402	STX10	Syntaxin-10	Non-raft	2	39/249	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00293402	STX10	Syntaxin-10	Raft	2	41/249	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
801	++	IPI00026128	STX11	Syntaxin-11	Non-raft	2	18/287	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
802	++++	IPI00013930	STX6	Syntaxin-6	Non-raft	4	83/255	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
		IPI00013930	STX6	Syntaxin-6	Raft	3	51/255	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
803	+++	IPI00289876	STX7	syntaxin 7	Non-raft	2	29/261	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
804	+++++	IPI00009225	STX8	Syntaxin-8	Non-raft	7	91/236	+++++	7.0	0.0	23.3	7	0	23.3	7	0	23.3
		IPI00009225	STX8	Syntaxin-8	Raft	4	60/236	+++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
805	+++	IPI00297626	STXBP3	Syntaxin-binding protein 3	Non-raft	4	55/592	+++	3.0	0.5	6.0	5	1	5.0	1	0	3.3
806	+++++	IPI00399142	SURF4	Surfeit 4	Non-raft	7	75/188	+++++	12.0	0.0	40.0	13	0	43.3	11	0	36.7
807	-	IPI00021302	SUSD2	Sushi domain-containing protein 2 precursor	Non-raft	5	71/822	-	1.5	2.0	0.8	2	4	0.5	1	0	3.3
808	-	IPI00018140	SYNCRIP	Isoform 1 of Heterogeneous nuclear ribonucleoprotein Q	Non-raft	3	34/623	+	1.5	1.0	1.5	2	2	1.0	1	0	3.3
		IPI00018140	SYNCRIP	Isoform 1 of Heterogeneous nuclear ribonucleoprotein Q	Raft	5	57/623	-	4.5	4.0	1.1	6	5	1.2	3	3	1.0
809	-	IPI00297910	TACSTD2	Tumor-associated calcium signal transducer 2 precursor	Non-raft	3	38/323	-	1.5	2.0	0.8	3	4	0.8	0	0	0.0
810	+	IPI00550363	TAGLN2	Transgelin-2	Non-raft	4	65/199	+	1.5	0.5	3.0	2	0	6.7	1	1	1.0
811	-	IPI00002232	TAOK1	Isoform 1 of Serine/threonine-protein kinase TAO1	Raft	2	21/1001	-	0.5	1.0	0.5	1	2	0.5	0	0	0.0
812	+++	IPI00646625	TAP1	transporter 1, ATP-binding cassette, sub-family B	Non-raft	3	51/808	+++	2.0	0.0	6.7	3	0	10.0	1	0	3.3
813	++	IPI00001382	TAP2	transporter 2, ATP-binding cassette, sub-family B isoform 2	Non-raft	2	19/653	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
814	+	IPI00329633	TARS	Threonyl-tRNA synthetase, cytoplasmic	Non-raft	10	123/723	+	5.0	3.0	1.7	9	4	2.3	1	2	0.5
815	++	IPI00333215	TCEA1	Isoform 1 of Transcription elongation factor A protein 1	Non-raft	2	26/301	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
816	+	IPI00290566	TCP1	T-complex protein 1 subunit alpha	Non-raft	12	180/556	+	8.0	2.5	3.2	11	5	2.2	5	0	16.7
817	+++++	IPI00022462	TFRC	Transferrin receptor protein 1	Non-raft	43	453/760	+++++	69.0	7.0	9.9	87	10	8.7	51	4	12.8
		IPI00022462	TFRC	Transferrin receptor protein 1	Raft	20	266/760	+++++	22.0	1.5	14.7	28	0	93.3	16	3	5.3
818	-	IPI00294578	TGM2	Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	Non-raft	13	206/687	-	10.5	11.0	1.0	14	14	1.0	7	8	0.9
819	-	IPI00300376	TGM3	Protein-glutamine gamma-glutamyltransferase E precursor	Non-raft	4	71/693	-	0.0	2.5	0.0	0	4	0.0	0	1	0.0
		IPI00300376	TGM3	Protein-glutamine gamma-glutamyltransferase E precursor	Raft	2	26/693	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
820	++	IPI00010737	THBD	Thrombomodulin precursor	Non-raft	2	21/575	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
821	-	IPI00296099	THBS1	Thrombospondin-1 precursor	Non-raft	3	38/1170	-	0.0	1.5	0.0	0	3	0.0	0	0	0.0
822	+	IPI00305374	THOC1	THO complex subunit 1	Raft	10	127/657	+	4.5	3.0	1.5	8	6	1.3	1	0	3.3
823	+	IPI00063729	THOC3	THO complex subunit 3	Raft	2	20/378	+	1.0	0.5	2.0	1	1	1.0	1	0	3.3
824	+	IPI00301252	THOC6	Isoform 3 of THO complex subunit 6 homolog	Raft	7	108/296	+	3.0	2.0	1.5	5	3	1.7	1	1	1.0
825	++	IPI00306516	TIMM44	Import inner membrane translocase subunit TIM44, mitochondrial precursor	Non-raft	2	25/452	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
826	-	IPI00643920	TKT	Transketolase	Non-raft	11	141/631	-	7.0	5.0	1.4	8	8	1.0	6	2	3.0
827	+	IPI00298994	TLN1	271 kDa protein	Non-raft	8	125/2541	-	1.5	3.5	0.4	2	5	0.4	1	2	0.5
		IPI00298994	TLN1	271 kDa protein	Raft	3	45/2541	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
828	++	IPI00021985	TM9SF4	Transmembrane 9 superfamily protein member 4	Non-raft	2	33/642	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
829	++++	IPI00009976	TMED1	Transmembrane emp24 domain-containing protein 1 precursor	Non-raft	4	48/227	++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
830	++	IPI00028055	TMED10	Transmembrane emp24 domain-containing protein 10 precursor	Non-raft	2	21/219	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
831	++	IPI00170706	TMEM2	Transmembrane protein 2	Non-raft	10	128/1383	++	6.5	2.0	3.3	9	4	2.3	4	0	13.3
832	+	IPI00299084	TMEM33	Transmembrane protein 33	Non-raft	3	38/247	+	4.0	1.5	2.7	4	1	4.0	4	2	2.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
833	++++	IPI00000612	TMEM50A	Transmembrane protein 50A	Raft	2	19/157	++++	4.5	0.0	15.0	7	0	23.3	2	0	6.7
834	+++	IPI00030530	TMEM55B	Isoform 1 of Transmembrane protein 55B	Non-raft	2	33/277	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
		IPI00030530	TMEM55B	Isoform 1 of Transmembrane protein 55B	Raft	4	54/277	+++	2.0	0.0	6.7	4	0	13.3	0	0	0.0
835	+++	IPI00399320	TMEM59	Transmembrane protein 59	Non-raft	2	26/323	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
		IPI00399320	TMEM59	Transmembrane protein 59	Raft	2	28/323	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
836	++++	IPI00006006	TMEM63A	Transmembrane protein 63A	Non-raft	5	49/807	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
837	++++	IPI00514538	TMEM63B	transmembrane protein 63B	Non-raft	4	43/832	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
		IPI00514538	TMEM63B	transmembrane protein 63B	Raft	5	54/832	++++	2.5	0.0	8.3	5	0	16.7	0	0	0.0
838	-	IPI00216230	TMPO	Lamina-associated polypeptide 2 isoform alpha	Raft	6	101/694	-	1.5	2.0	0.8	3	4	0.8	0	0	0.0
839	++++	IPI00304866	TNFAIP2	Tumor necrosis factor, alpha-induced protein 2	Non-raft	6	78/654	++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
840	+++++	IPI00021975	TNFRSF10A	Tumor necrosis factor receptor superfamily member 10A precursor	Non-raft	8	99/468	+++++	16.5	0.5	33.0	18	1	18.0	15	0	50.0
		IPI00021975	TNFRSF10A	Tumor necrosis factor receptor superfamily member 10A precursor	Raft	2	26/468	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
841	+++++	IPI00296379	TNFRSF10B	Isoform Long of Tumor necrosis factor receptor superfamily member 10B precursor	Non-raft	5	85/440	+++++	8.0	0.5	16.0	10	1	10.0	6	0	20.0
		IPI00296379	TNFRSF10B	Isoform Long of Tumor necrosis factor receptor superfamily member 10B precursor	Raft	5	79/440	+++++	5.5	0.0	18.3	6	0	20.0	5	0	16.7
842	++++	IPI00294516	TNFRSF10D	Tumor necrosis factor receptor superfamily member 10D precursor	Non-raft	2	41/386	++++	3.0	0.0	10.0	5	0	16.7	1	0	3.3
843	-	IPI00304589	TNKS1BP1	182 kDa tankyrase 1-binding protein	Raft	5	85/1729	-	1.0	1.5	0.7	2	3	0.7	0	0	0.0
844	-	IPI00169434	TNRC15	Hypothetical protein DKFZp686O20169	Raft	2	33/1299	-	0.5	1.0	0.5	1	2	0.5	0	0	0.0
845	+++	IPI00014053	TOMM40	Isoform 1 of Probable mitochondrial import receptor subunit TOM40 homolog	Non-raft	2	17/361	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
846	-	IPI00015602	TOMM70A	Mitochondrial precursor proteins import receptor	Non-raft	4	49/608	-	2.5	2.0	1.3	4	3	1.3	1	1	1.0
847	+++++	IPI00009111	TPBG	Trophoblast glycoprotein precursor	Non-raft	8	100/420	+++++	13.0	1.5	8.7	16	2	8.0	10	1	10.0
		IPI00009111	TPBG	Trophoblast glycoprotein precursor	Raft	2	33/420	++	1.0	0.0	3.3	0	0	0.0	2	0	6.7
848	+	IPI00465028	TPI1	Triosephosphate isomerase 1 variant	Non-raft	13	165/286	+	8.5	5.0	1.7	14	9	1.6	3	1	3.0
849	-	IPI00178083	TPM3	29 kDa protein	Non-raft	5	42/224	-	2.0	2.5	0.8	4	4	1.0	0	1	0.0
		IPI00178083	TPM3	29 kDa protein	Raft	3	34/224	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
850	-	IPI00030275	TRAP1	Heat shock protein 75 kDa, mitochondrial precursor	Non-raft	6	78/704	-	3.0	4.5	0.7	4	6	0.7	2	3	0.7
851	+++++	IPI00004324	TRAPPC3	Trafficking protein particle complex subunit 3	Non-raft	3	36/180	+++++	6.0	0.0	20.0	4	0	13.3	8	0	26.7
		IPI00004324	TRAPPC3	Trafficking protein particle complex subunit 3	Raft	3	36/180	++++	3.5	0.0	11.7	5	0	16.7	2	0	6.7
852	+	IPI00029629	TRIM25	Tripartite motif-containing protein 25	Non-raft	4	54/630	+	2.5	1.5	1.7	3	2	1.5	2	1	2.0
		IPI00029629	TRIM25	Tripartite motif-containing protein 25	Raft	9	119/630	+	5.5	3.0	1.8	8	5	1.6	3	1	3.0
853	-	IPI00438229	TRIM28	tripartite motif-containing 28 protein	Non-raft	6	84/835	-	1.0	2.0	0.5	2	2	1.0	0	2	0.0
		IPI00438229	TRIM28	tripartite motif-containing 28 protein	Raft	2	23/835	-	0.5	0.5	1.0	1	1	1.0	0	0	0.0
854	+++	IPI00165394	TSPAN14	Isoform 2 of Tetraspanin-14	Non-raft	2	28/253	+++	2.0	0.0	6.7	1	0	3.3	3	0	10.0
855	++	IPI00000736	TSPAN15	Tetraspanin-15	Non-raft	2	32/294	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
856	+++	IPI00024174	TSPAN4	Tetraspanin-4	Non-raft	2	33/238	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
857	++++	IPI00027437	TSPAN9	Tetraspanin-9	Non-raft	2	29/239	++++	2.5	0.0	8.3	2	0	6.7	3	0	10.0
858	++	IPI00023283	TTN	Isoform 2 of Titin	Raft	2	17/34258	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
859	+++++	IPI00877061	TTYH3	Isoform 3 of protein tweety homolog 3	Non-raft	2	29/352	+++++	5.0	0.0	16.7	5	0	16.7	5	0	16.7
860	-	IPI00180675	TUBA1A	Tubulin alpha-3 chain	Non-raft	16	219/451	-	10.5	9.0	1.2	11	8	1.4	10	10	1.0
861	-	IPI00387144	TUBA1B	Tubulin alpha-ubiquitous chain	Non-raft	17	233/451	-	16.0	14.0	1.1	17	14	1.2	15	14	1.1

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
		IPI00387144	TUBA1B	Tubulin alpha-ubiquitous chain	Raft	8	127/451	+	8.0	4.0	2.0	11	6	1.8	5	2	2.5
862	–	IPI00218343	TUBA1C	Tubulin alpha-6 chain	Non-raft	16	216/449	–	15.0	12.5	1.2	15	13	1.2	15	12	1.3
		IPI00218343	TUBA1C	Tubulin alpha-6 chain	Raft	5	84/449	+	6.0	3.0	2.0	7	4	1.8	5	2	2.5
863	+	IPI00007750	TUBA4A	Tubulin alpha-1 chain	Non-raft	11	160/448	+	7.5	4.0	1.9	15	8	1.9	0	0	0.0
864	+	IPI00646909	TUBA8	Tubulin alpha-8 chain	Non-raft	9	130/449	+	10.5	6.5	1.6	10	7	1.4	11	6	1.8
865	–	IPI00011654	TUBB	Tubulin beta-2 chain	Non-raft	20	293/444	–	18.5	15.0	1.2	20	19	1.1	17	11	1.5
		IPI00011654	TUBB	Tubulin beta-2 chain	Raft	12	165/444	–	7.0	8.0	0.9	7	10	0.7	7	6	1.2
866	–	IPI00013475	TUBB2A	tubulin, beta 2	Non-raft	16	127/445	–	11.0	9.0	1.2	11	10	1.1	11	8	1.4
867	–	IPI00007752	TUBB2C	Tubulin beta-2C chain	Non-raft	19	283/445	–	15.5	13.5	1.1	18	17	1.1	13	10	1.3
868	–	IPI00013683	TUBB3	Tubulin beta-3 chain	Non-raft	7	71/450	–	3.0	4.5	0.7	6	9	0.7	0	0	0.0
869	–	IPI00641706	TUBB6	46 kDa protein	Non-raft	7	76/409	–	2.5	2.0	1.3	5	4	1.3	0	0	0.0
870	+	IPI00027107	TUFM	Tu translation elongation factor, mitochondrial	Non-raft	3	38/455	+	2.0	1.0	2.0	3	1	3.0	1	1	1.0
871	+++	IPI00470779	TXLNA	Alpha-taxilin	Raft	3	38/546	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
872	+++++	IPI00395887	TXNDC1	Thioredoxin domain-containing protein 1 precursor	Non-raft	10	102/280	+++++	25.5	2.5	10.2	21	3	7.0	30	2	15.0
		IPI00395887	TXNDC1	Thioredoxin domain-containing protein 1 precursor	Raft	7	73/280	+++++	8.5	0.0	28.3	8	0	26.7	9	0	30.0
873	+++++	IPI00064193	TXNDC10	Isoform 1 of Protein disulfide-isomerase TXNDC10 precursor	Non-raft	8	131/454	+++++	7.0	0.5	14.0	6	1	6.0	8	0	26.7
874	+	IPI00329596	TXNDC14	CDNA PSEC0045 fis, clone NT2RP1001023	Non-raft	2	27/371	+	1.5	0.5	3.0	2	0	6.7	1	1	1.0
875	–	IPI00171438	TXNDC5	Thioredoxin domain-containing protein 5 precursor	Non-raft	3	34/432	–	2.0	1.5	1.3	3	2	1.5	1	1	1.0
		IPI00171438	TXNDC5	Thioredoxin domain-containing protein 5 precursor	Raft	3	19/432	–	0.5	1.0	0.5	1	0	3.3	0	2	0.0
876	+	IPI00554786	TXNRD1	Thioredoxin reductase 1, cytoplasmic precursor	Non-raft	13	185/499	+	8.0	5.0	1.6	10	6	1.7	6	4	1.5
877	+++	IPI00157820	TXNRD2	Isoform 2 of Thioredoxin reductase 2, mitochondrial precursor	Non-raft	2	30/522	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
878	–	IPI00000684	UAP1	Isoform AGX2 of UDP-N-acetylhexosamine pyrophosphorylase	Non-raft	2	26/522	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
879	+++++	IPI00645078	UBA1	Ubiquitin-activating enzyme E1	Non-raft	22	373/1058	+++++	17.0	3.0	5.7	22	5	4.4	12	1	12.0
880	++++	IPI00023234	UBA2	Ubiquitin-like 1-activating enzyme E1B	Non-raft	5	66/640	++++	2.5	0.0	8.3	4	0	13.3	1	0	3.3
881	+++	IPI00003949	UBE2N	Ubiquitin-conjugating enzyme E2 N	Non-raft	2	30/152	+++	2.0	0.0	6.7	2	0	6.7	2	0	6.7
		IPI00003949	UBE2N	Ubiquitin-conjugating enzyme E2 N	Raft	2	30/152	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
882	++++	IPI00026669	UBL3	Ubiquitin-like protein 3 precursor	Non-raft	3	26/117	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7
883	+++++	IPI00017227	UBTD1	Ubiquitin domain-containing protein 1	Non-raft	3	35/227	+++	1.5	0.0	5.0	2	0	6.7	1	0	3.3
		IPI00017227	UBTD1	Ubiquitin domain-containing protein 1	Raft	8	79/227	+++++	6.0	0.0	20.0	9	0	30.0	3	0	10.0
884	+++	IPI00157729	UBTD2	Ubiquitin domain-containing protein 2	Raft	3	35/234	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
885	+	IPI00172656	UBXD8	UBX domain-containing protein 8	Non-raft	4	59/445	+	2.5	1.5	1.7	2	1	2.0	3	2	1.5
886	+++++	IPI00018352	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	Non-raft	5	72/223	+++++	3.5	0.5	7.0	4	0	13.3	3	0	10.0
887	+	IPI00031420	UGDH	UDP-glucose 6-dehydrogenase	Non-raft	12	165/494	+	8.5	4.5	1.9	12	5	2.4	5	4	1.3
888	++++	IPI00034049	UPF1	Isoform 1 of Regulator of nonsense transcripts 1	Raft	7	85/1129	++++	3.5	0.5	7.0	7	1	7.0	0	0	0.0
889	++	IPI00004406	UPP1	Isoform 1 of Uridine phosphorylase 1	Non-raft	2	30/310	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
890	–	IPI00013847	UQCRC1	Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor	Non-raft	2	24/480	–	0.5	1.0	0.5	1	2	0.5	0	0	0.0
891	+	IPI00291946	USP10	Ubiquitin carboxyl-terminal hydrolase 10	Raft	6	105/798	+	3.5	2.0	1.8	4	2	2.0	3	2	1.5
892	–	IPI00219913	USP14	Ubiquitin carboxyl-terminal hydrolase 14	Non-raft	2	24/494	–	0.5	1.0	0.5	1	1	1.0	0	1	0.0
893	+++++	IPI00549343	VAMP3	Vesicle-associated membrane protein 3	Non-raft	9	77/100	+++++	15.5	0.0	51.7	14	0	46.7	17	0	56.7
		IPI00549343	VAMP3	Vesicle-associated membrane protein 3	Raft	5	41/100	+++++	4.5	0.0	15.0	5	0	16.7	4	0	13.3
894	++++	IPI00219648	VAMP4	Isoform 2 of Vesicle-associated membrane protein 4	Non-raft	3	34/140	++++	2.5	0.0	8.3	2	0	6.7	3	0	10.0
895	+++++	IPI00013236	VAMP7	Isoform 2 of Synaptobrevin-like protein 1	Non-raft	7	109/260	+++++	5.5	0.0	18.3	3	0	10.0	8	0	26.7
896	+++++	IPI00031195	VANGL1	Isoform 1 of Vang-like protein 1	Non-raft	8	139/524	++++	4.5	0.0	15.0	7	0	23.3	2	0	6.7
		IPI00031195	VANGL1	Isoform 1 of Vang-like protein 1	Raft	6	99/524	+++++	3.5	0.0	11.7	4	0	13.3	3	0	10.0

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
897	+	IPI00170692	VAPA	vesicle-associated membrane protein-associated protein A isoform 2	Non-raft	3	30/249	+	1.5	0.5	3.0	2	1	2.0	1	0	3.3
		IPI00170692	VAPA	vesicle-associated membrane protein-associated protein A isoform 2	Raft	2	14/249	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0
898	–	IPI00006211	VAPB	VAMP-associated protein B/C	Non-raft	2	28/243	–	0.5	0.5	1.0	1	1	1.0	0	0	0.0
899	–	IPI00000873	VAR5	Valyl-tRNA synthetase	Non-raft	9	121/1264	–	4.0	3.0	1.3	6	4	1.5	2	2	1.0
900	–	IPI00156689	VAT1	Synaptic vesicle membrane protein VAT-1 homolog	Non-raft	6	86/393	–	2.5	2.5	1.0	4	3	1.3	1	2	0.5
901	–	IPI00022774	VCP	Transitional endoplasmic reticulum ATPase	Non-raft	34	398/806	–	25.5	23.5	1.1	30	31	1.0	21	16	1.3
		IPI00022774	VCP	Transitional endoplasmic reticulum ATPase	Raft	3	37/806	–	1.0	1.0	1.0	2	2	1.0	0	0	0.0
902	–	IPI00216308	VDAC1	Voltage-dependent anion-selective channel protein 1	Non-raft	10	128/283	–	8.5	8.0	1.1	12	10	1.2	4	6	0.7
903	+	IPI00216026	VDAC2	Isoform 3 of Voltage-dependent anion-selective channel protein 2	Non-raft	13	192/294	+	15.0	9.5	1.6	20	12	1.7	10	7	1.4
		IPI00216026	VDAC2	Isoform 3 of Voltage-dependent anion-selective channel protein 2	Raft	3	32/294	–	1.0	1.0	1.0	2	1	2.0	0	1	0.0
904	+	IPI00031804	VDAC3	Isoform 1 of Voltage-dependent anion-selective channel protein 3	Non-raft	10	108/283	+	8.5	5.0	1.7	8	7	1.1	9	3	3.0
905	+	IPI00418471	VIM	Vimentin	Raft	15	195/466	+	11.0	4.0	2.8	19	7	2.7	3	1	3.0
906	–	IPI00024273	VLDLR	Isoform Long of Very low-density lipoprotein receptor precursor	Non-raft	2	25/873	–	0.0	1.0	0.0	0	2	0.0	0	0	0.0
907	++	IPI00018931	VPS35	Vacuolar protein sorting-associated protein 35	Non-raft	2	23/796	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
908	+	IPI00746165	WDR1	WD repeat-containing protein 1 isoform 1	Non-raft	3	42/606	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
909	++	IPI00220834	XRCC5	ATP-dependent DNA helicase 2 subunit 2	Non-raft	11	142/732	++	5.5	1.5	3.7	9	2	4.5	2	1	2.0
		IPI00220834	XRCC5	ATP-dependent DNA helicase 2 subunit 2	Raft	16	201/732	+	11.5	7.0	1.6	18	12	1.5	5	2	2.5
910	+	IPI00465430	XRCC6	70 kDa protein	Non-raft	8	101/609	+	4.0	2.5	1.6	7	4	1.8	1	1	1.0
		IPI00465430	XRCC6	70 kDa protein	Raft	8	116/609	++	4.0	1.0	4.0	6	0	20.0	2	2	1.0
911	–	IPI00657645	XRN1	Isoform 2 of 5'-3' exoribonuclease 1	Raft	3	30/1694	–	1.0	1.0	1.0	2	2	1.0	0	0	0.0
912	+	IPI00386208	YA61	Gastric-associated differentially-expressed protein YA61P	Non-raft	14	138/136	+	103.0	52.5	2.0	106	58	1.8	100	47	2.1
913	+++++	IPI00013981	YES1	Proto-oncogene tyrosine-protein kinase Yes	Non-raft	17	221/543	+++++	14.5	2.5	5.8	16	3	5.3	13	2	6.5
		IPI00013981	YES1	Proto-oncogene tyrosine-protein kinase Yes	Raft	26	342/543	+++++	25.0	3.0	8.3	30	4	7.5	20	2	10.0
914	++	IPI00216318	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide	Non-raft	5	75/246	++	2.0	0.5	4.0	4	1	4.0	0	0	0.0
915	+++	IPI00000816	YWHAE	14-3-3 protein epsilon	Non-raft	3	35/255	+++	1.5	0.0	5.0	4	0	13.3	0	0	0.0
		IPI00000816	YWHAE	14-3-3 protein epsilon	Raft	2	23/255	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
916	+++	IPI00220642	YWHAG	14-3-3 protein gamma	Non-raft	5	64/247	+++	2.5	0.5	5.0	5	1	5.0	0	0	0.0
		IPI00220642	YWHAG	14-3-3 protein gamma	Raft	2	25/247	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
917	++	IPI00216319	YWHAH	14-3-3 protein eta	Non-raft	2	25/246	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
918	+++	IPI00018146	YWHAQ	14-3-3 protein theta	Non-raft	3	31/245	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
919	+	IPI00021263	YWHAZ	14-3-3 protein zeta/delta	Non-raft	5	68/245	+	2.5	1.0	2.5	5	2	2.5	0	0	0.0
		IPI00021263	YWHAZ	14-3-3 protein zeta/delta	Raft	3	35/245	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
920	+	IPI00332936	ZC3HAV1	Isoform 2 of Zinc finger CCCH type antiviral protein 1	Non-raft	3	40/699	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
		IPI00332936	ZC3HAV1	Isoform 2 of Zinc finger CCCH type antiviral protein 1	Raft	8	132/699	–	4.0	3.5	1.1	7	7	1.0	1	0	3.3
921	+++	IPI00062698	ZDHHC12	Isoform 1 of Probable palmitoyltransferase ZDHHC12	Non-raft	2	22/267	+++	1.5	0.0	5.0	1	0	3.3	2	0	6.7
		IPI00062698	ZDHHC12	Isoform 1 of Probable palmitoyltransferase ZDHHC12	Raft	2	22/267	++	1.0	0.0	3.3	1	0	3.3	1	0	3.3
922	++	IPI00410663	ZDHHC13	Isoform 1 of Probable palmitoyltransferase ZDHHC13	Non-raft	2	25/622	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
923	++	IPI00410687	ZDHHC17	Huntingtin interacting protein 14	Non-raft	2	18/632	++	1.0	0.0	3.3	2	0	6.7	0	0	0.0
924	++++	IPI00398974	ZDHHC20	Isoform 1 of Probable palmitoyltransferase ZDHHC20	Non-raft	6	73/365	++++	5.5	0.0	18.3	9	0	30.0	2	0	6.7
		IPI00398974	ZDHHC20	Isoform 1 of Probable palmitoyltransferase ZDHHC20	Raft	2	38/365	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
925	+++++	IPI00328272	ZDHHC5	Isoform 1 of Probable palmitoyltransferase ZDHHC5	Non-raft	10	151/715	+++++	6.0	0.0	20.0	9	0	30.0	3	0	10.0
		IPI00328272	ZDHHC5	Isoform 1 of Probable palmitoyltransferase ZDHHC5	Raft	4	69/715	++++	3.0	0.0	10.0	4	0	13.3	2	0	6.7

No.	Prob. Both	Acc.Number	Gene Symbol	Description	Fraction	Uni. Pep.	Sequence Coverage	Prob. Each	Spectral Counts								
									Avg. EXP	Avg. CON	Avg. Ratio	1st Biol. Replicate			2nd Biol. Replicate		
												1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio
926	+++	IPI00008350	ZDHHC6	Isoform 1 of Probable palmitoyltransferase ZDHHC6	Non-raft	2	20/413	+++	1.5	0.0	5.0	3	0	10.0	0	0	0.0
927	+	IPI00333858	ZFR	117 kDa protein	Raft	2	26/1079	+	1.5	0.5	3.0	3	1	3.0	0	0	0.0
928	+	IPI00020513	ZYX	67 kDa protein	Non-raft	2	35/632	+	1.0	0.5	2.0	2	1	2.0	0	0	0.0

Category	Criterion	Avg. EXP	Avg. Ratio	1st EXP	1st Ratio	2nd EXP	2nd Ratio
Highly probable	+++++	≥6	≥3.3	≥3	≥2.5	≥3	≥2.5
Probable	++++	Any	≥7.0	Not satisfy the + + + + criterion			
	+++	Any	≥5.0 and <7.0				
	++	Any	≥3.3 and <5.0				
Others	+	Any	≥1.5 and <3.3				
	–	Any	<1.5				

- Note 1.** No. = Number (see the 1st column)
- Note 2.** Prob. Both = Probability in Both Fractions (see the 2nd column)
- Note 3.** Uni. Pep. = Unique Peptides (see the 7th column)
- Note 4.** Prot. Each = Probability in Each Fraction (see the 9th column)
- Note 5.** Avg. = Average (see the 10th~12th columns).
- Note 6.** To avoid division by zero, a value of 0.3 was substituted for CON spectral counts of 0 (see the 11th, 14th, and 17th columns) so that the ratios (see the 12th, 15th, and 18th columns) could be calculated.
- Note 7.** Proteins were assorted according to the Gene Symbols (see the 4th column).
- Note 8.** Highly probable S-acylated proteins were highlighted with yellow (see the 3rd~5th columns).
- Note 9.** Potential false-positives were highlighted with cyan (see the 3rd~5th columns).
- Note 10:** S-acylated proteins were purified from about 1.25 mg non-raft and 1.25 mg raft proteins, respectively.

Table S2. Highly probable S-acylated proteins identified by the protein-based procedure.

Acc.Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protein Family		Other Evidence	
IPI00065486	ABCB6	CDNA FLJ32464 fis, clone SKNMC1000251, highly similar to Homo sapiens MT-ABC transporter (MTABC) mRNA								
IPI00006675	ABCC4	Multidrug resistance-associated protein 4								
IPI00013897	ADAM10	ADAM 10 precursor				2.3 : 0				
IPI00008982	ALDH18A1	Isoform Long of Delta 1-pyrroline-5-carboxylate synthetase								
IPI00103467	ALDH1B1	Aldehyde dehydrogenase X, mitochondrial precursor					ALDH	8120000		
IPI00018031	ALDH3B1	Isoform 1 of Aldehyde dehydrogenase 3B1					ALDH	8120000		
IPI00030431	ANTXR1	Isoform 1 of Anthrax toxin receptor 1 precursor	16401723			2.7 : 0				
IPI00036552	ANTXR2	Isoform 2 of Anthrax toxin receptor 2 precursor	16401723							
IPI00255653	ATP11A	Probable phospholipid-transporting ATPase 1H								
IPI00240793	ATP11B	Probable phospholipid-transporting ATPase 1F				4.8 : 0				
IPI00303476	ATP5B	ATP synthase subunit beta, mitochondrial precursor								
IPI00001891	AUP1	Isoform Long of Ancient ubiquitous protein 1 precursor				8.5 : 0				
IPI00002406	BCAM	Lutheran blood group glycoprotein precursor								
IPI00016670	C11orf59	FLJ20625 protein				21 : 2.3				
IPI00166051	C14orf24	Uncharacterized protein C14orf24								
IPI00303401	C1orf75	FLJ10874 protein				2.0 : 0				
IPI00176427	CADM4	TSLC1-like 2		19092927	rat					
IPI00020984	CANX	Calnexin precursor		18350545	mouse	95 : 11				
IPI00009236	CAV1	Caveolin 1	11451957				Caveolin			
IPI00298851	CD151	CD151 antigen	11907260				Tetraspanin			
IPI00297160	CD44	CD44 antigen isoform 4 precursor	16945930							
IPI00219852	CD46	Isoform B of Membrane cofactor protein precursor								
IPI00215998	CD63	CD63 antigen	11959120							
IPI00031713	CD70	Tumor necrosis factor ligand superfamily member 7					TNF receptor	17159908		
IPI00000190	CD81	CD81 antigen	11959120			1.3 : 0	Tetraspanin			
IPI00215997	CD9	CD9 antigen	11959120				Tetraspanin			
IPI00016786	CDC42	Isoform 2 of Cell division control protein 42 homolog precursor		19092927	rat		Rho			
IPI00290039	CDCP1	Isoform 1 of CUB domain-containing protein 1 precursor								
IPI00141318	CKAP4	Isoform 1 of Cytoskeleton-associated protein 4	18296695							
IPI00007364	CLDN3	Claudin-3					Claudin	15769849		
IPI00011284	COMT	Isoform Membrane-bound of Catechol O-methyltransferase								
IPI00181294	CSNK1G3	Isoform 1 of Casein kinase I isoform gamma-3				2.7 : 0	Casein kinase	14668479		
IPI00009633	CTDSP1	Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1				2.0 : 0				
IPI00182469	CTNND1	Isoform 1AB of Catenin delta-1		19092927	rat					
IPI00019146	CXADR	Isoform 1 of Coxsackievirus and adenovirus receptor precursor	12021372							
IPI00385987	DAGLB	Isoform 1 of Sn1-specific diacylglycerol lipase beta				10 : 0.8				
IPI00217282	DCUN1D3	DCN1, defective in cullin neddylation 1, domain containing 3								
IPI00023780	DNAJC5	Isoform 2 of DnaJ homolog subfamily C member 5		9761715	rat	2.7 : 0				
IPI00402231	DNAJC5	Isoform 1 of DnaJ homolog subfamily C member 5		9761715	rat					
IPI00028931	DSG2	desmoglein 2 preproprotein				2.7 : 0				
IPI00216760	ECE1	Isoform C of Endothelin-converting enzyme 1	10359648							
IPI00470711	EFR3A	Hypothetical protein DKFZp781J0562								
IPI00010187	ELOVL1	Elongation of very long chain fatty acids protein 1							Fatty acid elongation	

Acc.Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protein Family		Other Evidence	
IPI00438286	ERBB2IP	Isoform 1 of Protein LAP2	18498353			7.2 : 0				
IPI00010338	F3	Tissue factor precursor	3166978							
IPI00412592	FAM108B1	chromosome 9 open reading frame 77 isoform 2				14.8 : 0				
IPI00303318	FAM49B	Protein FAM49B				6.5 : 0.7				
IPI00026781	FASN	Fatty acid synthase							Fatty acid elongation	
IPI00021048	FER1L3	Isoform 1 of Myoferlin								
IPI00027438	FLOT1	Flotillin-1		12370178	mouse	23.5 : 0				
IPI00029625	FLOT2	Flotillin-2		14599293	rat	6.3 : 0				
IPI00020228	FZD6	Frizzled-6 precursor								
IPI00219018	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase							Palmitoylation in vitro	16128592
IPI00217952	GFPT1	Isoform 1 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1								
IPI00305551	GNA11	Guanine nucleotide-binding protein subunit alpha-11	9175863			13.5 : 0	G protein alpha			
IPI00328744	GNA12	Guanine nucleotide-binding protein alpha-12 subunit	9485474				G protein alpha			
IPI00290928	GNA13	Guanine nucleotide-binding protein alpha-13 subunit	10747909			17.5 : 0	G protein alpha			
IPI00337415	GNAI1	Guanine nucleotide-binding protein G(i), alpha-1 subunit		8484716	Rat		G protein alpha			
IPI00748145	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2		8484716	Rat	23.8 : 1	G protein alpha			
IPI00220578	GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha				19.5 : 0	G protein alpha	8484716		
IPI00288947	GNAQ	Guanine nucleotide binding protein	8227063			38.3 : 0	G protein alpha			
IPI00219835	GNAS	Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short		8484716	Rat	9.8 : 0	G protein alpha			
IPI00514055	GNAS	Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short		8484716	Rat		G protein alpha			
IPI00644936	GNAS	Guanine nucleotide-binding protein G-s-alpha-3		8484716	Rat		G protein alpha			
IPI00480022	GOLGA7	Isoform 1 of Golgin subfamily A member 7	14522980			5.5 : 0				
IPI00004962	GOLIM4	golgi phosphoprotein 4								
IPI00217481	GPR126	Developmentally regulated G-protein-coupled receptor beta 1					GPCR	15250498		
IPI00022624	GPRC5A	Retinoic acid-induced protein 3								
IPI00471955	HLA-B	HLA class I histocompatibility antigen, B-50 alpha chain precursor					Homologous to HLA B-7	17785801		
IPI00473131	HLA-C	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	17785801							
IPI00008475	HMGCS1	Hydroxymethylglutaryl-CoA synthase, cytoplasmic							azidopalmitate labeling	17971398
IPI00000006	HRAS	GTPase HRas precursor	10504264			8.7 : 0				
IPI00017726	HSD17B10	hydroxyacyl-Coenzyme A dehydrogenase, type II isoform 1				2.5 : 0.3			azidopalmitate labeling	17971398
IPI00027422	ITGB4	Isoform Beta-4C of Integrin beta-4 precursor	14517202							
IPI00016014	ITM2C	Isoform 1 of Integral membrane protein 2C								
IPI00029046	KIAA0152	Protein KIAA0152 precursor				33.5 : 0				
IPI00423568	KRAS	Isoform 2A of GTPase KRas	3023817			10.8 : 0				
IPI00014172	LAPTM4A	Lysosomal-associated transmembrane protein 4A								
IPI00219219	LGALS1	Galectin-1								
IPI00221240	LNPEP	Isoform 2 of Leucyl-cystinyl aminopeptidase				14.7 : 0.3				
IPI00427739	LRRC1	Isoform 1 of Leucine-rich repeat-containing protein 1				4.3 : 0				

Acc.Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protein Family		Other Evidence	
IPI00409640	LSR	Isoform 1 of Lipolysis-stimulated lipoprotein receptor							Cystein-rich domain	
IPI00298625	LYN	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	10669752							
IPI00025049	M6PR	Cation-dependent mannose-6-phosphate receptor precursor		8647889	bovine					
IPI00016334	MCAM	Isoform 1 of Cell surface glycoprotein MUC18 precursor								
IPI00218398	MMP14	Matrix metalloproteinase-14 precursor	15946988							
IPI00174976	MPP5	Isoform 1 of MAGUK p55 subfamily member 5					MAGUK p55	1713685		
IPI00303280	MPP6	MAGUK p55 subfamily member 6				2.3 : 0	MAGUK p55	1713685		
IPI00017515	MREG	DSU protein				3.8 : 0				
IPI00328715	MTDH	Protein LYRIC				45 : 0				
IPI00385172	MUC1	Mucin 1, transmembrane	16507569							
IPI00021983	NCSTN	Isoform 1 of Nicastrin precursor	19028695							
IPI00005107	NPC1	Niemann-Pick C1 protein precursor								
IPI00000005	NRAS	GTPase NRas precursor	2661017							
IPI00299594	NRP1	Isoform 1 of Neuropilin-1 precursor								
IPI00017231	NRSN2	Protein C20orf98								
IPI00022674	OSMR	oncostatin M receptor								
IPI00329572	PACSIN3	49 kDa protein								
IPI00020124	PI4K2A	Phosphatidylinositol 4-kinase type II		19211550	rat	30.0 : 0				
IPI00291068	PI4K2B	Phosphatidylinositol 4-kinase type-II beta		17927563	bovine	4.5 : 0				
IPI00005181	PLSCR1	Phospholipid scramblase 1	12564925				PLSCR			
IPI00216127	PLSCR3	Phospholipid scramblase 3					PLSCR	12564925		
IPI00419585	PPIA	Peptidyl-prolyl cis-trans isomerase A								
IPI00028077	PSEN1	Isoform 1 of Presenilin-1				1.3 : 0				
IPI00179964	PTBP1	Isoform 1 of Polypyrimidine tract-binding protein 1				6.7 : 0.5				
IPI00022048	PTGFRN	Prostaglandin F2 receptor negative regulator precursor								
IPI00168812	PTK7	PTK7 protein tyrosine kinase 7 isoform d precursor				3.2 : 0				
IPI00032903	PTRH2	Peptidyl-tRNA hydrolase 2, mitochondrial precursor				19 : 0				
IPI00219425	PVR	Isoform Beta of Poliovirus receptor precursor								
IPI00022661	PVRL2	Isoform Delta of Poliovirus receptor-related protein 2 precursor								
IPI00016513	RAB10	Ras-related protein Rab-10					Ras-related			
IPI00291928	RAB14	Ras-related protein Rab-14					Ras-related			
IPI00005719	RAB1A	RAB1A, member RAS oncogene family					Ras-related			
IPI00008964	RAB1B	Ras-related protein Rab-1B				16.0 : 4.0	Ras-related			
IPI00300096	RAB35	Ras-related protein Rab-35					Ras-related			
IPI00016339	RAB5C	Ras-related protein Rab-5C				3.5 : 0.5	Ras-related			
IPI00028481	RAB8A	Ras-related protein Rab-8A					Ras-related			
IPI00217519	RALA	Ras-related protein Ral-A					Ras-related			
IPI00004397	RALB	Ras-related protein Ral-B					Ras-related			
IPI00019346	RAP2A	Ras-related protein Rap-2a				22 : 0	Highly homologous to RAP2B	18582561		
IPI00018364	RAP2B	Ras-related protein Rap-2b precursor	18582561			37 : 0				
IPI00009607	RAP2C	Ras-related protein Rap-2c precursor				34 : 0	Ras-related			
IPI00000041	RHOB	Rho-related GTP-binding protein RhoB precursor	1400319				Rho			
IPI00017342	RHOG	Rho-related GTP-binding protein RhoG precursor					Rho			
IPI00024933	RPL12	60S ribosomal protein L12				4.2 : 0				

Acc.Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protein Family		Other Evidence	
IPI00550021	RPL3	60S ribosomal protein L3				6.3 : 0				
IPI00301271	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor								
IPI00179330	RPS27A	ubiquitin and ribosomal protein S27a precursor								
IPI00020418	RRAS	Ras-related protein R-Ras	12890755			5.2 : 0				
IPI00012512	RRAS2	Ras-related protein R-Ras2					Homologous to RRAS	12890755		
IPI00061267	RSPRY1	Ring finger and SPRY domain containing 1				3.2 : 0				
IPI00005129	SCAMP1	Isoform 1 of Secretory carrier-associated membrane protein 1		19092927	rat	8.7 : 0	SCAMP			
IPI00218850	SCAMP2	Secretory carrier-associated membrane protein 2				7.8 : 0	SCAMP			
IPI00306382	SCAMP3	Isoform 1 of Secretory carrier-associated membrane protein 3				21 : 2.8	SCAMP			
IPI00056310	SCAMP4	Secretory carrier-associated membrane protein 4					SCAMP			
IPI00177968	SCARB1	Isoform 1 of Scavenger receptor class B member 1								
IPI00217766	SCARB2	Lysosome membrane protein 2								
IPI00410666	SCRIB	Isoform 3 of Protein LAP4				8.3 : 0	LAP	18498353		
IPI00019472	SLC1A5	Neutral amino acid transporter B(0)				10 : 1.1				
IPI00007188	SLC25A5	ADP/ATP translocase 2								
IPI00384867	SLC35B2	Isoform 2 of Adenosine 3'-phospho 5'-phosphosulfate transporter 1				3.2 : 0				
IPI00410034	SLC38A2	Putative 40-9-1 protein				5.0 : 0				
IPI00221393	SLC44A1	Isoform 1 of Choline transporter-like protein 1								
IPI00027728	SLC7A1	High-affinity cationic amino acid transporter 1				4.3 : 0				
IPI00010438	SNAP23	Isoform SNAP-23a of Synaptosomal-associated protein 23	10329400			25 : 1.5				
IPI00219682	STOM	Erythrocyte band 7 integral membrane protein	10338112			3.0 : 0				
IPI00009225	STX8	Syntaxin-8	18980942			8.8 : 0.3	Syntaxin			
IPI00399142	SURF4	Surfeit 4				7.8 : 0				
IPI00022462	TFRC	Transferrin receptor protein 1	2398066			71 : 16				
IPI00021975	TNFRSF10A	Tumor necrosis factor receptor superfamily member 10A precursor	19090789				TNF receptor	17159908		
IPI00296379	TNFRSF10B	Isoform Long of Tumor necrosis factor receptor superfamily member 10B precursor					TNF receptor	17159908		
IPI00009111	TPBG	Trophoblast glycoprotein precursor								
IPI00004324	TRAPPC3	Trafficking protein particle complex subunit 3	15692564							
IPI00877061	TTYH3	Isoform 3 of protein tweety homolog 3								
IPI00395887	TXNDC1	Thioredoxin domain-containing protein 1 precursor				63 : 0				
IPI00064193	TXNDC10	Isoform 1 of Protein disulfide-isomerase TXNDC10 precursor				9.0 : 0				
IPI00017227	UBTD1	Ubiquitin domain-containing protein 1								
IPI00549343	VAMP3	Vesicle-associated membrane protein 3				2.7 : 0.3	Synaptobrevin	10845776		
IPI00013236	VAMP7	Isoform 2 of Synaptobrevin-like protein 1					Synaptobrevin	10845776		
IPI00031195	VANGL1	Isoform 1 of Vang-like protein 1				13 : 0				
IPI00013981	YES1	Proto-oncogene tyrosine-protein kinase Yes		7980442	monkey	4.0 : 0				
IPI00328272	ZDHHC5	Isoform 1 of Probable palmitoyltransferase ZDHHC5				4.7 : 0			DHHC protein	

Note 1. Acc. Number = Accession Number (see the 1st column)

Note 2. Spectral count ratio of candidate palmitoyl proteins (PMID: 19137006) (see the 6th column)

Table S3. Probable S-acylated proteins identified by the protein-based procedure.

Prob. Both	Acc. Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protei Family	
++	IPI00002230	AADACL1	Arylacetamide deacetylase-like 1				2.2 : 0		
++	IPI00008338	ABCC1	Isoform 2 of Multidrug resistance-associated protein 1						
++	IPI00001539	ACAA2	3-ketoacyl-CoA thiolase, mitochondrial						
++	IPI00003807	ACP2	Lysosomal acid phosphatase precursor						
++	IPI00029737	ACSL4	Isoform Long of Long-chain-fatty-acid--CoA ligase 4						
+++	IPI00029606	ADAM17	Isoform B of ADAM 17 precursor						
+++	IPI00025057	ADAR	Isoform 2 of Double-stranded RNA-specific adenosine deaminase						
++++	IPI00019141	AGPAT1	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha				17 : 0		
+++	IPI00385128	AGPAT7	Isoform 1 of 1-acyl-sn-glycerol-3-phosphate acyltransferase eta						
+++	IPI00856045	AHNAK2	Isoform 1 of protein AHNAK2						
++	IPI00000690	AIFM1	Isoform 1 of Programmed cell death protein 8, mitochondrial precursor						
++	IPI00015102	ALCAM	CD166 antigen precursor						
+++	IPI00019888	ALDH5A1	Succinate semialdehyde dehydrogenase, mitochondrial precursor					ALDH	8120000
+++	IPI00024990	ALDH6A1	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor					ALDH	8120000
+++	IPI00555692	ANXA4	ANXA4 protein						
++	IPI00016621	AP2A2	AP-2 complex subunit alpha-2						
++++	IPI00005163	ARL15	ARFRP2 protein				2.7 : 0		
+++	IPI00007426	ARL6IP5	PRA1 family protein 3						
+++	IPI00167074	ARL6IP6	Phosphonoformate immuno-associated protein 1				3.0 : 0		
+++	IPI00013698	ASAH1	Acid ceramidase precursor						
++	IPI00420014	ASCC3L1	U5 small nuclear ribonucleoprotein 200 kDa helicase				4.7 : 1.2		
+++	IPI00554777	ASNS	Asparagine synthetase						
++++	IPI00177661	ATP13A3	PREDICTED: similar to Probable cation-transporting ATPase 13A3 (ATPase family homolog up-regulated in senescence cells 1) isoform 2				3.5 : 0		
++	IPI00220473	ATP2C1	Isoform 2 of Calcium-transporting ATPase type 2C member 1						
++	IPI00219291	ATP5J2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2 isoform 2b						
++	IPI00007611	ATP5O	ATP synthase O subunit, mitochondrial precursor				2.8 : 0.3		
++	IPI00024368	ATP9A	Isoform Long of Probable phospholipid-transporting ATPase IIA						
++	IPI00456359	ATXN2L	Isoform 1 of Ataxin-2-like protein						
+++	IPI00215767	B4GALT1	Isoform Long of Beta-1,4-galactosyltransferase 1				2.5 : 0		
+++	IPI00000643	BAG2	BAG family molecular chaperone regulator 2						
++++	IPI00033075	BAT5	Protein BAT5				11 : 0		
++++	IPI00019835	BCL2L12	Isoform 1 of Bcl-2-related proline-rich protein						
++++	IPI00030959	C13orf1	24 kDa protein						
++++	IPI00006980	C14orf166	Protein C14orf166						
++	IPI00056357	C19orf10	Uncharacterized protein C19orf10 precursor						
++	IPI00024913	C21orf33	Isoform Long of ES1 protein homolog, mitochondrial precursor						
++++	IPI00550440	C2orf18	Uncharacterized protein C2orf18 precursor						
++++	IPI00024618	C3orf37	UPF0361 protein DC12						
++	IPI00550571	C5orf15	Keratinocytes-associated transmembrane protein 2 precursor						
+++	IPI00031617	C6orf125	Protein C6orf125						
++	IPI00007067	C9orf19	Golgi-associated plant pathogenesis-related protein 1						
++	IPI00012429	C9orf5	Isoform 2 of Protein C9orf5						
+++	IPI00395627	CACYBP	Isoform 1 of Calyculin-binding protein						
+++	IPI00008274	CAP1	Adenylyl cyclase-associated protein 1						

Prob. Both	Acc. Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protei Family	
++	IPI00643994	CAPN5	CDNA FLJ46245 fis, clone TESTI4020596, highly similar to Homo sapiens calpain 5						
+++	IPI00026185	CAPZB	Isoform 1 of F-actin capping protein subunit beta						
++++	IPI00514301	CASK	Peripheral plasma membrane protein CASK						
++++	IPI00019870	CAV2	Isoform Alpha of Caveolin-2					Caveolin	
++	IPI00410093	CCDC69	coiled-coil domain containing 69						
++++	IPI00334743	CCNY	Isoform 2 of Cyclin fold protein 1				5.3 : 0		
++++	IPI00185371	CCNYL1	CDNA FLJ40432 fis, clone TESTI2039227				2.0 : 0		
++++	IPI00410488	CD276	Isoform 1 of CD276 antigen precursor						
+++	IPI00000059	CD58	LFA-3						
++++	IPI00024973	CDC42SE2	CDC42 small effector 2				2.2 : 0		
+++	IPI00015713	CDKAL1	CDK5 regulatory subunit associated protein 1-like 1						
++	IPI00045511	CLCC1	Mid-1-related chloride channel 1 isoform 1						
++++	IPI00000691	CLDN1	Claudin-1					Claudin	15769849
++++	IPI00059710	CLDN23	Claudin-23					Claudin	15769849
++++	IPI00072743	CLDND1	Isoform 1 of Claudin domain-containing protein 1						
++	IPI00024776	CLGN	Calmegin precursor				4.7 : 0		
++	IPI00001960	CLIC4	Chloride intracellular channel protein 4						
++	IPI00430813	CNBP	Isoform 2 of Cellular nucleic acid-binding protein						
+++	IPI00220993	CNP	Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase						
++	IPI00007058	CORO1B	Coronin-1B						
++++	IPI00027078	CPD	Carboxypeptidase D precursor	12643288			8.0 : 0		
++	IPI00032038	CPT1A	Isoform 1 of Carnitine O-palmitoyltransferase I, liver isoform				4.0 : 0		
+++	IPI00219823	CSNK1G1	Isoform 1S of Casein kinase I isoform gamma-1				2.3 : 0	Casein kinase	14668479
+++	IPI00297767	CSNK1G2	Casein kinase I isoform gamma-2						
+++	IPI00024826	CTDSPL	CTD small phosphatase-like protein						
++	IPI00215948	CTNNA1	Isoform 1 of Catenin alpha-1						
++	IPI00019994	CXorf15	Gamma-taxilin						
++++	IPI00303954	CYB5B	cytochrome b5 outer mitochondrial membrane precursor						
++	IPI00102928	CYB5D2	Cytochrome b5 domain containing 2						
++++	IPI00337800	DAAM1	Isoform 1 of Disheveled-associated activator of morphogenesis 1				2.5 : 0		
++	IPI00003406	DBN1	Drebrin						
++	IPI00300567	DCI	Isoform 1 of 3,2-trans-enoyl-CoA isomerase, mitochondrial precursor						
++	IPI00030320	DDX6	Probable ATP-dependent RNA helicase DDX6						
+++	IPI00003482	DECR1	2,4-dienoyl-CoA reductase, mitochondrial precursor						
++	IPI00299076	EBAG9	Receptor-binding cancer antigen expressed on SiSo cells (Fragment)				9.7 : 0		
+++	IPI00024993	ECHS1	Enoyl-CoA hydratase, mitochondrial precursor						
++++	IPI00376317	EDC4	autoantigen RCD8				2.8 : 0		
++	IPI00023048	EEF1D	Elongation factor 1-delta				2.0 : 0.3		
++++	IPI00304661	EEPD1	hypothetical protein LOC80820						
+++	IPI00016910	EIF3C	Eukaryotic translation initiation factor 3 subunit 8				2.8 : 0.5		
++	IPI00654777	EIF3F	Eukaryotic translation initiation factor 3 subunit 5						
++	IPI00290460	EIF3G	Eukaryotic translation initiation factor 3 subunit 4						
+++	IPI00647650	EIF3H	Eukaryotic translation initiation factor 3 subunit 3						
+++	IPI00033143	EIF3K	Eukaryotic translation initiation factor 3 subunit 12						
++++	IPI00022648	EIF5	Eukaryotic translation initiation factor 5						
+++	IPI00006935	EIF5A2	Eukaryotic translation initiation factor 5A-2						
++	IPI00010105	EIF6	Eukaryotic translation initiation factor 6						

Prob. Both	Acc. Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protei Family	
+++	IPI00006438	ERGIC3	Isoform 1 of Endoplasmic reticulum-Golgi intermediate compartment protein 3				4.5 : 0		
+++	IPI00024911	ERP29	Endoplasmic reticulum protein ERp29 precursor						
+++	IPI00429191	ETF1	Eukaryotic peptide chain release factor subunit 1						
++	IPI00015905	EXOSC2	Exosome complex exonuclease RRP4						
++	IPI00073602	EXOSC6	homolog of yeast mRNA transport regulator 3						
++	IPI00747290	FAM108C1	Isoform 2 of abhydrolase domain-containing protein FAM108C1				2.2 : 0		
++	IPI00039626	FAM120A	Isoform D of UPF0318 protein FAM120A						
++	IPI00021923	FAM3C	Protein FAM3C precursor						
++++	IPI00174757	FBXL20	F-box/LRR-repeat protein 20						
++	IPI00013281	FKRP	Fukutin-related protein						
+++	IPI00301987	FLJ20323	hypothetical protein FLJ20323						
++	IPI00016250	FXR2	Fragile X mental retardation syndrome-related protein 2						
++	IPI00025273	GART	Isoform Long of Trifunctional purine biosynthetic protein adenosine-3						
++++	IPI00220281	GNAO1	Guanine nucleotide-binding protein G(o) subunit alpha 1		8484716	Rat	12 : 0	G alpha	
++++	IPI00027497	GPI	Glucose-6-phosphate isomerase						
++++	IPI00099883	GPRC5C	G-protein coupled receptor family C group 5 member C precursor					GPCR	15250498
++	IPI00332155	GPRIN1	Isoform 1 of G protein-regulated inducer of neurite outgrowth 1						
+++	IPI00011913	HNRNPA0	Heterogeneous nuclear ribonucleoprotein A0						
+++	IPI00419373	HNRPA3	Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3						
++	IPI00171903	HNRPM	heterogeneous nuclear ribonucleoprotein M isoform a						
++++	IPI00289819	IGF2R	Cation-independent mannose-6-phosphate receptor precursor				9.3 : 1.3		
++	IPI00056478	IGSF8	Isoform 1 of Immunoglobulin superfamily member 8 precursor				11 : 0		
++	IPI00788962	IL10RB	Protein						
++	IPI00006774	IL27RA	Interleukin-27 receptor subunit alpha						
+++	IPI00297124	IL6ST	Isoform 1 of Interleukin-6 receptor beta chain precursor						
+++	IPI00554541	ILVBL	ilvB (bacterial acetolactate synthase)-like isoform 1						
++	IPI00032262	INPP5A	Type I inositol-1,4,5-trisphosphate 5-phosphatase						
++	IPI00215995	ITGA3	Isoform Alpha-3A of Integrin alpha-3 precursor						
++++	IPI00010697	ITGA6	Isoform Alpha-6X1X2B of Integrin alpha-6 precursor						
+++	IPI00031821	ITM2B	Integral membrane protein 2B						
+++	IPI00006130	KIAA0494	Uncharacterized calcium-binding protein KIAA0494				4.7 : 0		
+++	IPI00217007	KIAA2013	Novel protein				4.3 : 0		
+++	IPI00004503	LAMP1	lysosomal-associated membrane protein 1						
+++	IPI00103994	LARS	Leucyl-tRNA synthetase, cytoplasmic				6.8 : 1.3		
++	IPI00395993	LAT2	Isoform 1 of Linker for activation of T-cells family member 2						
++	IPI00394952	LCK	lymphocyte-specific protein tyrosine kinase precursor	9092949			75 : 1.1		
+++	IPI00020007	LMBRD1	LMBR1 domain containing 1						
++++	IPI00293336	LOC153364	similar to metallo-beta-lactamase superfamily protein				2.8 : 0		
+++	IPI00373972	LOC388564	PREDICTED: hypothetical protein						
+++	IPI00291695	LOC493869	CDNA FLJ23636 fis, clone CAS07176						
+++	IPI00414231	LRP10	Isoform 1 of Low-density lipoprotein receptor-related protein 10 precursor					LDL receptor	18378904
++	IPI00021027	LRP12	Low-density lipoprotein receptor-related protein 12 precursor					LDL receptor	18378904
++	IPI00170935	LRRC47	Leucine-rich repeat-containing protein 47						
+++	IPI00007321	LYPLA1	Isoform 1 of Acyl-protein thioesterase 1						
+++	IPI00090807	METTL7B	Methyltransferase-like protein 7B precursor						
++	IPI00002236	MFGE8	Lactadherin precursor						
++++	IPI00395906	MGC59937	Similar to RIKEN cDNA 2310002J15 gene						

Prob. Both	Acc. Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protei Family	
+++	IPI00215610	MPP1	55 kDa erythrocyte membrane protein	1713685					
+++	IPI00219365	MSN	Moesin						
+++	IPI00102685	MYADM	Myeloid-associated differentiation marker				1.3 : 0		
++	IPI00023748	NACA	Nascent polypeptide-associated complex subunit alpha						
++	IPI00306960	NARS	Asparaginyl-tRNA synthetase, cytoplasmic						
++	IPI00444262	NCL	CDNA FLJ45706 fis, clone FEBRA2028457, highly similar to Nucleolin						
++	IPI00470649	NCLN	Isoform 1 of Nicalin precursor						
+++	IPI00012235	NDFIP1	Isoform 1 of NEDD4 family-interacting protein 1				4.7 : 0.7		
+++	IPI00012048	NME1	Nucleoside diphosphate kinase A						
+++	IPI00304596	NONO	Non-POU domain-containing octamer-binding protein						
++	IPI00017672	NP	CDNA FLJ25678 fis, clone TST04067, highly similar to PURINE NUCLEOSIDE PHOSPHORYLASE						
++	IPI00026216	NPEPPS	Puromycin-sensitive aminopeptidase						
++	IPI00220740	NPM1	Isoform 2 of Nucleophosmin						
++++	IPI00012069	NQO1	NAD(P)H dehydrogenase [quinone] 1						
++	IPI00008524	PABPC1	Isoform 1 of Polyadenylate-binding protein 1						
+++	IPI00020464	PAG1	Phosphoprotein associated with glycosphingolipid-enriched microdomains 1		12626544	Mouse			
++++	IPI00301023	PALM	Isoform 1 of Paralemmin		19299482	monkey			
+++	IPI00073769	PALM2	A kinase						
++	IPI00018873	PBEF1	Isoform 1 of Nicotinamide phosphoribosyltransferase						
++++	IPI00869136	PCNXL3	Isoform 1 of Pecanex-like protein 3						
+++	IPI00306301	PDHA1	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor						
+++	IPI00293189	PERP	Isoform 1 of p53 apoptosis effector related to PMP-22						
+++	IPI00549725	PGAM1	Phosphoglycerate mutase 1						
+++	IPI00017334	PHB	Prohibitin						
++	IPI00021076	PKP4	Isoform Long of Plakophilin-4						
+++	IPI00152701	PLCD3	phospholipase C delta 3						
++	IPI00012865	PLD1	Isoform PLD1A of Phospholipase D1		11121416	rat			
+++	IPI00030362	PLP2	Proteolipid protein 2						
++	IPI00165506	POLDIP2	Polymerase delta-interacting protein 2						
++	IPI00005705	PPP1CC	Isoform Gamma-1 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit						
++	IPI00063273	PPP1R16A	Protein phosphatase 1 regulatory subunit 16A						
++	IPI00026994	PRAF2	PRA1 family protein 2				7.7 : 0		
++++	IPI00009276	PROCR	Endothelial protein C receptor precursor						
++	IPI00004968	PRPF19	Pre-mRNA-processing factor 19				2.2 : 0.3		
++	IPI00030770	PSMG1	Isoform 1 of Down syndrome critical region protein 2						
+++	IPI00103525	PSPC1	paraspeckle protein 1 isoform alpha						
++	IPI00298347	PTPN11	Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11						
++++	IPI00107831	PTPRF	Receptor-type tyrosine-protein phosphatase F precursor						
+++	IPI00011651	PTPRG	Receptor-type tyrosine-protein phosphatase gamma precursor						
++++	IPI00023974	PTTG1IP	Pituitary tumor-transforming gene 1 protein-interacting protein precursor						
+++	IPI00023504	RAB3A	Ras-related protein Rab-3A					Ras-related	
+++	IPI00300562	RAB3B	Ras-related protein Rab-3B					Ras-related	
+++	IPI00032808	RAB3D	Ras-related protein Rab-3D					Ras-related	
++	IPI00016891	RAB6B	Ras-related protein Rab-6B						

Prob. Both	Acc. Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protei Family	
++	IPI00010271	RAC1	Isoform A of Ras-related C3 botulinum toxin substrate 1 precursor						
++++	IPI00643041	RAN	GTP-binding nuclear protein Ran					Ras-related	
+++	IPI00031755	RCE1	CAAX prenyl protease 2						
++++	IPI00024670	REEP5	Receptor expression-enhancing protein 5						
++++	IPI00216890	RELL1	Similar to expressed sequence AA536743						
++++	IPI00103867	RFFL	Isoform 1 of Rififylin						
++	IPI00005250	RGS17	Regulator of G-protein signaling 17					RGS	8986788
++	IPI00028108	RGS19	Regulator of G-protein signaling 19	8986788			3.5 : 0	RGS	
++++	IPI00008802	RGS20	Isoform 6 of Regulator of G-protein signaling 20						
++++	IPI00027500	RHOA	Transforming protein RhoA precursor					Rho	
+++	IPI00027434	RHOC	Rho-related GTP-binding protein RhoC precursor					Rho	
+++	IPI00023511	RNF167	RING finger protein 167 precursor						
+++	IPI00010405	ROR1	Isoform Long of Tyrosine-protein kinase transmembrane receptor ROR1 precursor						
+++	IPI00026627	RP2	Protein XRP2	10942419					
++	IPI00020127	RPA1	Replication protein A 70 kDa DNA-binding subunit						
+++	IPI00412579	RPL10A	60S ribosomal protein L10a				0.7 : 0		
+++	IPI00304612	RPL13A	60S ribosomal protein L13a						
++	IPI00375511	RPL15	26 kDa protein						
+++	IPI00215719	RPL18	60S ribosomal protein L18						
++	IPI00182533	RPL28	60S ribosomal protein L28						
+++	IPI00219156	RPL30	60S ribosomal protein L30						
++	IPI00029731	RPL35A	60S ribosomal protein L35a						
++	IPI00000494	RPL5	60S ribosomal protein L5				3.2 : 0.3		
+++	IPI00012772	RPL8	60S ribosomal protein L8						
++	IPI00031691	RPL9	60S ribosomal protein L9						
++++	IPI00025091	RPS11	40S ribosomal protein S11						
+++	IPI00221091	RPS15A	40S ribosomal protein S15a						
++	IPI00221093	RPS17	40S ribosomal protein S17				14 : 3.0		
++	IPI00012493	RPS20	40S ribosomal protein S20						
++	IPI00419880	RPS3A	40S ribosomal protein S3a				3.8 : 0.5		
++	IPI00008433	RPS5	40S ribosomal protein S5				5.0 : 0.3		
++	IPI00013415	RPS7	40S ribosomal protein S7						
+++	IPI00221088	RPS9	40S ribosomal protein S9				3.7 : 0		
++	IPI00023101	RQCD1	Homo sapiens protein involved in sexual development, complete cds						
++	IPI00021766	RTN4	Isoform 1 of Reticulon-4				12 : 2.7		
++	IPI00298289	RTN4	Isoform 2 of Reticulon-4						
++	IPI00021187	RUVBL1	Isoform 1 of RuvB-like 1						
++	IPI00329600	SCCPDH	Probable saccharopine dehydrogenase				3.5 : 0		
+++	IPI00106642	SDF2L1	Dihydropyrimidinase-like 2						
+++	IPI00006865	SEC22B	Vesicle-trafficking protein SEC22b						
++	IPI00218922	SEC63	Translocation protein SEC63 homolog						
++	IPI00216139	SEPT6	septin 6 isoform A						
++++	IPI00033025	SEPT7	Septin-7						
+++	IPI00413817	SERINC1	Serine incorporator 1						
+++	IPI00166444	SFT2D3	Vesicle transport protein SFT2C				1.7 : 0		
++	IPI00009368	SFXN1	Sideroflexin-1						
++	IPI00394753	SLC11A2	Isoform 1 of Natural resistance-associated macrophage protein 2						

Prob. Both	Acc. Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protei Family	
++++	IPI00006666	SLC16A3	Monocarboxylate transporter 4						
++++	IPI00375452	SLC19A1	Folate transporter 1						
++++	IPI00032107	SLC26A2	Sulfate transporter						
++	IPI00024787	SLC27A2	Very-long-chain acyl-CoA synthetase						
++	IPI00550382	SLC29A1	Equilibrative nucleoside transporter 1						
+++	IPI00179969	SLC2A6	CDNA FLJ90355 fis, clone NT2RP2003469, moderately similar to Solute carrier family 2, facilitated glucose transporter, member 6						
++++	IPI00784764	SLC30A1	solute carrier family 30 (zinc transporter), member 1						
++	IPI00100585	SLC39A1	Zinc transporter ZIP1						
+++	IPI00293074	SLC44A2	Isoform 2 of Choline transporter-like protein 2						
+++	IPI00043883	SLC46A1	Isoform 1 of Heme carrier protein 1						
+++	IPI00383597	SLC4A2	Isoform A of Anion exchange protein 2					Homologous to SLC4A1	1885574
++++	IPI00031822	SLC5A6	Sodium-dependent multivitamin transporter				4.8 : 0		
++++	IPI00100858	SLCO4A1	Isoform 1 of Solute carrier organic anion transporter family member 4A1						
++	IPI00472939	SPCS2	Signal peptidase complex subunit 2						
+++	IPI00012913	SPRY2	SPRY2 protein						
++++	IPI00012434	STARD3NL	Isoform 1 of MLN64 N-terminal domain homolog						
++	IPI00005846	STEAP1	Six transmembrane epithelial antigen of prostate 1						
+++	IPI00334190	STOML2	Stomatin-like protein 2				3.8 : 0	Stomatin-like	10338112
++	IPI00293402	STX10	Syntaxin-10				2.0 : 0	Syntaxin	15973437
++	IPI00026128	STX11	Syntaxin-11					Syntaxin	15973437
++++	IPI00013930	STX6	Syntaxin-6		19092927	rat	6.8 : 0	Syntaxin	15973437
+++	IPI00289876	STX7	syntaxin 7	18980942			2.7 : 0	Syntaxin	15973437
+++	IPI00297626	STXBP3	Syntaxin-binding protein 3						
+++	IPI00646625	TAP1	transporter 1, ATP-binding cassette, sub-family B				7.0 : 0		
++	IPI00001382	TAP2	transporter 2, ATP-binding cassette, sub-family B isoform 2						
++	IPI00333215	TCEA1	Isoform 1 of Transcription elongation factor A protein 1						
++	IPI00010737	THBD	Thrombomodulin precursor						
++	IPI00306516	TIMM44	Import inner membrane translocase subunit TIM44, mitochondrial precursor						
++	IPI00021985	TM9SF4	Transmembrane 9 superfamily protein member 4						
++++	IPI00009976	TMED1	Transmembrane emp24 domain-containing protein 1 precursor				2.7 : 0		
++	IPI00028055	TMED10	Transmembrane emp24 domain-containing protein 10 precursor						
++	IPI00170706	TMEM2	Transmembrane protein 2						
++++	IPI00000612	TMEM50A	Transmembrane protein 50A						
+++	IPI00030530	TMEM55B	Isoform 1 of Transmembrane protein 55B				3.0 : 0		
+++	IPI00399320	TMEM59	Transmembrane protein 59						
++++	IPI00006006	TMEM63A	Transmembrane protein 63A				1.0 : 0		
++++	IPI00514538	TMEM63B	transmembrane protein 63B						
++++	IPI00304866	TNFAIP2	Tumor necrosis factor, alpha-induced protein 2						
++++	IPI00294516	TNFRSF10D	Tumor necrosis factor receptor superfamily member 10D precursor					TNF receptor	17159908
+++	IPI00014053	TOMM40	Isoform 1 of Probable mitochondrial import receptor subunit TOM40 homolog				6.2 : 0.8		
+++	IPI00165394	TSPAN14	Isoform 2 of Tetraspanin-14					Tetraspanin	11907260
++	IPI00000736	TSPAN15	Tetraspanin-15					Tetraspanin	11907260
+++	IPI00024174	TSPAN4	Tetraspanin-4					Tetraspanin	11907260
++++	IPI00027437	TSPAN9	Tetraspanin-9					Tetraspanin	11907260
++	IPI00023283	TTN	Isoform 2 of Titin						

Prob. Both	Acc. Number	Gene Symbol	Description	Known Human	Known Other Species		17-ODYA	Protei Family	
+++	IPI00470779	TXLNA	Alpha-taxilin						
+++	IPI00157820	TXNRD2	Isoform 2 of Thioredoxin reductase 2, mitochondrial precursor						
++++	IPI00026669	UBL3	Ubiquitin-like protein 3 precursor						
+++	IPI00157729	UBTD2	Ubiquitin domain-containing protein 2						
++++	IPI00034049	UPF1	Isoform 1 of Regulator of nonsense transcripts 1						
++	IPI00004406	UPP1	Isoform 1 of Uridine phosphorylase 1						
++++	IPI00219648	VAMP4	Isoform 2 of Vesicle-associated membrane protein 4				2.8 : 0	Synaptobrevin	
++	IPI00018931	VPS35	Vacuolar protein sorting-associated protein 35						
++	IPI00220834	XRCC5	ATP-dependent DNA helicase 2 subunit 2						
++	IPI00216318	YWHAB	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide						
+++	IPI00000816	YWHAE	14-3-3 protein epsilon						
+++	IPI00220642	YWHAG	14-3-3 protein gamma				4.0 : 0		
++	IPI00216319	YWHAH	14-3-3 protein eta						
+++	IPI00018146	YWHAQ	14-3-3 protein theta						
+++	IPI00062698	ZDHHC12	Isoform 1 of Probable palmitoyltransferase ZDHHC12					DHHC protein	
++	IPI00410663	ZDHHC13	Isoform 1 of Probable palmitoyltransferase ZDHHC13					DHHC protein	
++	IPI00410687	ZDHHC17	Huntingtin interacting protein 14				4.3 : 0	DHHC protein	
++++	IPI00398974	ZDHHC20	Isoform 1 of Probable palmitoyltransferase ZDHHC20				4.8 : 0	DHHC protein	
+++	IPI00008350	ZDHHC6	Isoform 1 of Probable palmitoyltransferase ZDHHC6				5.3 : 0	DHHC protein	

Note 1: Prob. Both = Probability in both fractions (see the 1st column)

Note 2: Spectral count ratio of candidate palmitoyl proteins (PMID: 19137006) (see the 7th column)

Table S4. S-acylation sites cannot be confidently localized on a large scale by using the protein-based procedure.

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
1	MALGTLALVLAL C R	Non-raft	0.5	0.0	1.67	1	0	0	0	ABCB6	IPI00065486	CDNA FLJ32464 fis, clone SKNMC1000251, highly similar to Homo sapiens MT-ABC transporter (MTABC) mRNA	50			
2	C PEALFQPSFLGMES C GIHETTFNSIMK	Non-raft	1.0	0.5	2.00	2	1	0	0	ACTB	IPI00021439	Actin, cytoplasmic 1	257	16453612	-	Dictyosteliu m
		Raft	1.0	0.5	2.00	2	1	0	0	ACTB	IPI00021439	Actin, cytoplasmic 1	257			
		Non-raft	1.0	0.5	2.00	2	1	0	0	ACTG1	IPI00021440	Actin, cytoplasmic 2	257	16453612	-	Dictyosteliu m
		Raft	1.0	0.5	2.00	2	1	0	0	ACTG1	IPI00021440	Actin, cytoplasmic 2	257			
3	C PEALFQPSFLGMES C GIHETTFNSIMK	Raft	0.5	0.0	1.67	1	0	0	0	ACTB	IPI00021439	Actin, cytoplasmic 1	272			
		Raft	0.5	0.0	1.67	1	0	0	0	ACTG1	IPI00021440	Actin, cytoplasmic 2	272			
4	L C YVALDFEQEMATAASSSSLEK	Non-raft	0.5	1.0	0.50	1	2	0	0	ACTB	IPI00021439	Actin, cytoplasmic 1	217			
		Raft	1.0	0.5	2.00	2	1	0	0	ACTB	IPI00021439	Actin, cytoplasmic 1	217			
		Non-raft	0.5	1.0	0.50	1	2	0	0	ACTG1	IPI00021440	Actin, cytoplasmic 2	217			
		Raft	1.0	0.5	2.00	2	1	0	0	ACTG1	IPI00021440	Actin, cytoplasmic 2	217			
5	DDDIAALVVDNGSGM C K	Non-raft	2.0	3.5	0.57	3	4	1	3	ACTB	IPI00021439	Actin, cytoplasmic 1	17			
		Raft	4.0	2.5	1.60	4	3	4	2	ACTB	IPI00021439	Actin, cytoplasmic 1	17			
6	EEEIAALVIDNGSGM C K	Non-raft	2.5	3.0	0.83	4	4	1	2	ACTG1	IPI00021440	Actin, cytoplasmic 2	17			
		Raft	2.5	1.5	1.67	4	1	1	2	ACTG1	IPI00021440	Actin, cytoplasmic 2	17			
7	I C DQWDNLGALTQK	Raft	0.5	0.0	1.67	1	0	0	0	ACTN1	IPI00013508	Alpha-actinin-1	480			
8	FSL C SIR	Non-raft	0.5	0.0	1.67	0	0	1	0	ADAM10	IPI00013897	ADAM 10 precursor	435			
9	TITLQPGSP C NDFR	Non-raft	0.5	0.0	1.67	1	0	0	0	ADAM10	IPI00013897	ADAM 10 precursor	632			
10	N C QFETAQKK	Non-raft	0.5	0.0	1.67	1	0	0	0	ADAM17	IPI00029606	Isoform B of ADAM 17 precursor	525			
11	LVDAGEE C D CGTPK	Non-raft	0.5	0.0	1.67	1	0	0	0	ADAM9	IPI00440932	Isoform 1 of ADAM 9 precursor	428			
12	LVDAGEE C D CGTPK	Non-raft	0.0	0.5	0.00	0	1	0	0	ADAM9	IPI00440932	Isoform 1 of ADAM 9 precursor	430			
13	AYGTGFVG C CLR	Non-raft	0.0	0.5	0.00	0	1	0	0	AGRN	IPI00374563	Agrin precursor	2016			
14	ALANSLA C QGK	Non-raft	0.5	1.0	0.50	1	1	0	1	ALDOA	IPI00465439	Fructose-bisphosphate aldolase A	339			
15	ALSDHHIYLEGTLLKPNMVTPGHA C TQK	Non-raft	0.5	0.0	1.67	1	0	0	0	ALDOA	IPI00465439	Fructose-bisphosphate aldolase A	240			
16	C PLLKPWALTFSYGR	Non-raft	0.5	0.0	1.67	0	0	1	0	ALDOA	IPI00465439	Fructose-bisphosphate aldolase A	290			
17	YAS I C QQNGIVPIVEPEILPDGDHDLKR	Non-raft	0.0	1.0	0.00	0	1	0	1	ALDOA	IPI00465439	Fructose-bisphosphate aldolase A	178			
18	TVAA C NLPIVR	Non-raft	0.0	1.0	0.00	0	0	0	2	AMBP	IPI00022426	AMBP protein precursor	287			
		Raft	0.0	0.5	0.00	0	0	0	1	AMBP	IPI00022426	AMBP protein precursor	287			
19	GDLENAFLNLV C IQNKPLYFADR	Non-raft	1.5	0.0	5.00	1	0	2	0	ANXA2	IPI00418169	annexin A2 isoform 1	280			
20	GLGTDEDSLIE I C SR	Non-raft	0.5	0.0	1.67	1	0	0	0	ANXA2	IPI00418169	annexin A2 isoform 1	151			
		Raft	0.5	0.5	1.00	1	1	0	0	ANXA2	IPI00418169	annexin A2 isoform 1	151			
		Non-raft	1.0	0.0	3.33	2	0	0	0	ANXA2P2	IPI00334627	Similar to annexin A2 isoform 1	133			
21	STVHEIL C K	Raft	1.0	0.0	3.33	1	0	1	0	ANXA2	IPI00418169	annexin A2 isoform 1	27			
22	L C SESPDNVVSTTGFSIK	Non-raft	1.0	0.0	3.33	0	0	2	0	ARL15	IPI00005163	ARFRP2 protein	53			
23	Y C AGEENWVDSR	Non-raft	0.5	0.0	1.67	0	0	1	0	ATP11A	IPI00255653	Probable phospholipid-transporting ATPase 1H	14			
24	NYLEPGKE C VQPATK	Non-raft	0.5	0.5	1.00	1	1	0	0	ATP2A2	IPI00219078	Isoform SERCA2B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	997			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
25	SMSVYCTPNKPSR	Non-raft	0.5	0.5	1.00	1	1	0	0	ATP2A2	IPI00219078	Isoform SERCA2B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	498			
26	VGEATETALTCLVEK	Non-raft	0.5	0.5	1.00	1	1	0	0	ATP2A2	IPI00219078	Isoform SERCA2B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	447			
27	VSFYQLSHFLQCK	Non-raft	0.5	0.0	1.67	1	0	0	0	ATP2A2	IPI00219078	Isoform SERCA2B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	875			
28	LLSCVLGPR	Non-raft	0.5	0.0	1.67	1	0	0	0	BAT5	IPI00033075	Protein BAT5	7			
29	EGDEVTLIC SAR	Non-raft	0.5	0.0	1.67	1	0	0	0	BCAM	IPI00002406	Lutheran blood group glycoprotein precursor	473			
30	EGDTVQLLCR	Non-raft	1.0	0.0	3.33	2	0	0	0	BCAM	IPI00002406	Lutheran blood group glycoprotein precursor	291			
31	GQSGTYGCRVEDYDAADDVQLSK	Non-raft	0.5	0.0	1.67	1	0	0	0	BCAM	IPI00002406	Lutheran blood group glycoprotein precursor	337			
32	LVLAEAQVGDERDYV CVVR	Non-raft	1.0	0.0	3.33	1	0	1	0	BCAM	IPI00002406	Lutheran blood group glycoprotein precursor	125			
33	LVELFC SR	Non-raft	0.5	0.0	1.67	1	0	0	0	BCL2L12	IPI00019835	Isoform 1 of Bcl-2-related proline-rich protein	254			
34	TPCNAGTFSQPEK	Raft	0.5	0.0	1.67	1	0	0	0	BUB3	IPI00013468	Mitotic checkpoint protein BUB3	129			
35	ATSVLCCLR	Non-raft	1.0	0.0	3.33	1	0	1	0	C13orf1	IPI00030959	24 kDa protein	7/8			
36	YLRDVNC PFK	Raft	0.5	0.0	1.67	1	0	0	0	C14orf166	IPI00006980	Protein C14orf166	69			
37	AATSTLSVCDFLGEK	Non-raft	0.5	0.0	1.67	1		0		C14orf24	IPI00166051	Uncharacterized protein C14orf24	114			
38	CESAPGCGVWQRPVIDNPNYK	Non-raft	1.5	0.0	5.00	1	0	2	0	CANX	IPI00020984	Calnexin precursor	360	18350545	503/504	Mouse
39	CESAPGCGVWQRPVIDNPNYK	Non-raft	1.0	0.0	3.33	2	0	0	0	CANX	IPI00020984	Calnexin precursor	366			
40	CGEDYKLHFIFR	Non-raft	0.5	0.0	1.67	0	0	1	0	CANX	IPI00020984	Calnexin precursor	194			
41	SFLIEIQCISR	Non-raft	0.5	0.0	1.67	0	0	1	0	CAV1	IPI00009236	caveolin 1	143	11451957	133/143/156	Human
		Raft	0.5	0.0	1.67	1	0	0	0	CAV1	IPI00009236	caveolin 1	143			
42	CFSSVSLQLSQD	Non-raft	0.5	0.0	1.67	0	0	1	0	CAV2	IPI00019870	Isoform Alpha of Caveolin-2	151			
		Raft	1.0	0.0	3.33	1	0	1	0	CAV2	IPI00019870	Isoform Alpha of Caveolin-2	151			
43	SVTDVIIAPLC TSVGR	Non-raft	0.5	0.0	1.67	0	0	1	0	CAV2	IPI00019870	Isoform Alpha of Caveolin-2	145			
		Raft	1.5	0.0	5.00	1	0	2	0	CAV2	IPI00019870	Isoform Alpha of Caveolin-2	145			
44	TCLMVLPSVQTIWK	Non-raft	1.0	0.0	3.33	0	0	2	0	CAV2	IPI00019870	Isoform Alpha of Caveolin-2	122			
		Raft	0.5	0.0	1.67	0	0	1	0	CAV2	IPI00019870	Isoform Alpha of Caveolin-2	122			
45	SQEAGGRVVPDSCCK	Non-raft	0.5	0.0	1.67	1	0	0	0	CD151	IPI00298851	CD151 antigen	184	11907260	11/15/242/243	
46	TVVALCGQR	Non-raft	2.0	0.0	6.67	1	0	3	0	CD151	IPI00298851	CD151 antigen	192			
47	ALSIGFETCR	Non-raft	0.5	0.0	1.67	0	0	1	0	CD44	IPI00297160	CD44 antigen isoform 4 precursor	28	16945930	286/295	
48	YSISRTEAADLCK	Non-raft	0.5	0.0	1.67	1	0	0	0	CD44	IPI00297160	CD44 antigen isoform 4 precursor	53			
49	AIHKEGCV EK	Non-raft	0.5	0.0	1.67	1	0	0	0	CD63	IPI00215998	CD63 antigen	191	11959120	-	
50	HHPTTLAVGICSPASR	Non-raft	1.0	0.0	3.33	2	0	0	0	CD70	IPI00031713	Tumor necrosis factor ligand superfamily member 7	133			
51	LSFHQGC TIASQR	Non-raft	1.0	0.0	3.33	2	0	0	0	CD70	IPI00031713	Tumor necrosis factor ligand superfamily member 7	151			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
52	RRPYG C VLR	Non-raft	0.5	0.0	1.67	1	0	0	0	CD70	IPI00031713	Tumor necrosis factor ligand superfamily member 7	17			
53	AIHYALN CC GLAGGVEQFISD C PK	Non-raft	0.5	0.0	1.67	1	0	0	0	CD9	IPI00215997	CD9 antigen	152/153/167	11959120	9/78/79/87/218/219	Human
54	AIHYALN CC GLAGGVEQFISD C PK	Non-raft	2.5	0.0	8.33	2	0	3	0	CD9	IPI00215997	CD9 antigen	152			
55	AIHYALN CC GLAGGVEQFISD C PK	Non-raft	1.5	0.0	5.00	0	0	3	0	CD9	IPI00215997	CD9 antigen	152/153			
56	AIHYALN CC GLAGGVEQFISD C PK	Non-raft	1.0	0.0	3.33	0	0	2	0	CD9	IPI00215997	CD9 antigen	167			
57	AIHYALN CC GLAGGVEQFISD C PK	Non-raft	0.5	0.0	1.67	0	0	1	0	CD9	IPI00215997	CD9 antigen	152/167			
58	YVE C SALTQK	Non-raft	0.5	0.5	1.00	1	0	0	1	CDC42	IPI00016786	Isoform 2 of Cell division control protein 42 homolog precursor	157			
59	C LEDDEVQKMR	Non-raft	0.5	0.0	1.67	1	0	0	0	CLDN1	IPI00000691	Claudin-1	107			
60	GFLNQPVDELQGLWDM C R	Raft	0.5	0.0	1.67	1	0	0	0	CLDN23	IPI00059710	Claudin-23	53			
61	IGN C PFSQR	Non-raft	0.5	0.0	1.67	1	0	0	0	CLIC1	IPI00010896	Chloride intracellular channel protein 1	24			
		Non-raft	0.5	0.0	1.67	1	0	0	0	CLIC4	IPI00001960	Chloride intracellular channel protein 4	35			
62	GTVLLADNV C PGAPDFLAHVR	Non-raft	0.5	0.0	1.67	1	0	0	0	COMT	IPI00011284	Isoform Membrane-bound of Catechol O-methyltransferase	223			
63	LITIEINPD C AAITQR	Non-raft	0.5	0.0	1.67	0	0	1	0	COMT	IPI00011284	Isoform Membrane-bound of Catechol O-methyltransferase	145			
64	YLPDTLLLE C GLLR	Non-raft	0.5	0.0	1.67	0	0	1	0	COMT	IPI00011284	Isoform Membrane-bound of Catechol O-methyltransferase	207			
65	C DLISIPK	Non-raft	0.5	0.0	1.67	1	0	0	0	CORO1C	IPI00008453	Coronin-1C	473			
		Raft	0.5	1.0	0.50	1	1	0	1	CORO1C	IPI00008453	Coronin-1C	473			
66	GLDVNK C EIAR	Raft	0.5	0.5	1.00	1	1	0	0	CORO1C	IPI00008453	Coronin-1C	383			
67	SIKDT C NQDER	Raft	0.5	0.5	1.00	1	1	0	0	CORO1C	IPI00008453	Coronin-1C	509			
68	VTWDSS C AVNPR	Raft	0.5	0.0	1.67	0	0	1	0	CORO1C	IPI00008453	Coronin-1C	92			
69	SILSSFF CC FR	Non-raft	0.5	0.0	1.67	0	0	1	0	CTDSPL	IPI00024826	CTD small phosphatase-like protein. Splice isoform 2	123/124			
70	HIEWESVLNTAG C LR	Non-raft	0.5	0.0	1.67	0	0	1	0	CTNND1	IPI00182469	Isoform 1AB of Catenin delta-1	533			
71	YQEAAPNVANNTGPHAAS C FGAK	Non-raft	1.5	0.0	5.00	1	0	2	0	CTNND1	IPI00182469	Isoform 1AB of Catenin delta-1	618			
		Raft	0.5	0.0	1.67	1	0	0	0	CTNND1	IPI00182469	Isoform 1AB of Catenin delta-1	618			
72	AKGETAYL C PK	Non-raft	0.5	0.0	1.67	1	0	0	0	CXADR	IPI00019146	Isoform 1 of Coxsackievirus and adenovirus receptor precursor	41	12021372	259/260	Human
73	C YVDGSEEIGSDFK	Non-raft	1.0	0.0	3.33	0	0	2	0	CXADR	IPI00019146	Isoform 1 of Coxsackievirus and adenovirus receptor precursor	146			
74	VGSDQ C LLR	Non-raft	2.0	0.0	6.67	3	0	1	0	CXADR	IPI00019146	Isoform 1 of Coxsackievirus and adenovirus receptor precursor	223			
75	FG CC SAAHYSAK	Non-raft	0.5	0.0	1.67	1	0	0	0	DAGLB	IPI00385987	Isoform 1 of Sn1-specific diacylglycerol lipase beta	610/611			
76	AISADSIDG C AR	Raft	0.5	0.0	1.67	1	0	0	0	DCUN1D3	IPI00217282	DCN1, defective in cullin neddylation 1, domain containing 3	163			
77	QDLGGT C VNEG C IPTK	Non-raft	0.5	0.0	1.67	1	0	0	0	DERP12	IPI00382990	DERP12	50			
		Raft	1.5	0.5	3.00	2	0	1	1	DERP12	IPI00382990	DERP12	50			
78	QDLGGT C VNEG C IPTK	Raft	2.5	2.0	1.25	3	3	2	1	DERP12	IPI00382990	DERP12	45			
79	QDLGGT C VNEG C IPTK	Raft	1.5	0.5	3.00	2	0	1	1	DERP12	IPI00382990	DERP12	45/50			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
80	LAAQSCALSLVR	Raft	0.0	0.5	0.00	0	1	0	0	DHX9	IPI00844578	ATP-dependent RNA helicase A	242			
81	HQGVMMVGMGQKDCYVGDEAQS	Raft	0.0	0.5	0.00	0	1	0	0	DKFZp686D0972	IPI00003269	hypothetical protein LOC345651	53			
82	IHSDCAANQQVITYR	Non-raft	0.0	1.0	0.00	0	2	0	0	DSG1	IPI00025753	Desmoglein-1 precursor	77			
83	TLAEVCLGQK	Raft	0.5	0.0	1.67	0	0	1	0	DSG2	IPI00028931	desmoglein 2 preproprotein	840			
84	CLNNYMIWNLVR	Non-raft	0.5	0.0	1.67	1	0	0	0	ECE1	IPI00216760	Isoform C of Endothelin-converting enzyme 1	372	10359648	42	Human
85	FCVSDTENNLGFALGPMFVK	Non-raft	0.5	0.0	1.67	0	0	1	0	ECE1	IPI00216760	Isoform C of Endothelin-converting enzyme 1	419			
86	ICPVETLVEEAIQCAEK	Non-raft	0.5	0.0	1.67	1	0	0	0	ECHS1	IPI00024993	Enoyl-CoA hydratase, mitochondrial precursor	213			
87	NMITGTSQADCAVLIVAAGVGEFEAGISK	Non-raft	1.0	0.0	3.33	0	0	2	0	EEF1A1	IPI00396485	Elongation factor 1-alpha 1	111			
		Non-raft	1.0	0.0	3.33	0	0	2	0	EEF1A2	IPI00014424	Elongation factor 1-alpha 2	111			
88	WFLTINQPQFR	Non-raft	1.0	0.0	3.33	1	0	1	0	EEF1G	IPI00000875	Elongation factor 1-gamma	194			
		Raft	1.0	0.5	2.00	1	1	1	0	EEF1G	IPI00000875	Elongation factor 1-gamma	194			
89	KIWCFGPDGTGPNILTDITK	Non-raft	0.5	0.0	1.67	0	0	1	0	EEF2	IPI00186290	Elongation factor 2	651			
90	LMETIYLVEIQCEQVVGGIYGLNR	Non-raft	0.5	0.0	1.67	0	0	1	0	EEF2	IPI00186290	Elongation factor 2	751			
91	TFCQLIDPIFK	Non-raft	1.0	1.0	1.00	1	1	1	1	EEF2	IPI00186290	Elongation factor 2	350			
92	YVEPIEDVPCGNIVGLVGVDQFLVK	Non-raft	0.5	0.5	1.00	1	1	0	0	EEF2	IPI00186290	Elongation factor 2	466			
93	IVLTNPVCTEVGEK	Non-raft	0.5	0.0	1.67	1	0	0	0	EIF2S3	IPI00297982	Eukaryotic translation initiation factor 2 subunit 3	434			
94	SFDVNKPGCEVDDLKGGVAGGSILK	Raft	0.5	0.0	1.67	1	0	0	0	EIF2S3	IPI00297982	Eukaryotic translation initiation factor 2 subunit 3	269			
95	VNQIGSVTESIQACK	Non-raft	1.0	0.5	2.00	1	1	1	0	ENO1	IPI00465248	enolase 1	357			
		Non-raft	1.0	0.5	2.00	1	1	1	0	ENO3	IPI00218474	Beta-enolase	357			
96	QLFNCQSLHK	Non-raft	0.5	0.0	1.67	1	0	0	0	ERBB2IP	IPI00438286	Isoform 1 of Protein LAP2	68	18498353	14/16	Human
97	LSCAYSGFSSPR	Non-raft	0.0	0.5	0.00	0	1	0	0	F11R	IPI00001754	Junctional adhesion molecule A precursor	50			
98	TYCFDAFPNIDK	Non-raft	1.0	0.0	3.33	2	0	0	0	FAM108B1	IPI00412592	chromosome 9 open reading frame 77 isoform 2	210			
99	VLTCITDLEQGNFFLDFENAQPTSEKEIYNQVNVVLK	Non-raft	1.5	0.0	5.00	2	0	1	0	FAM49B	IPI00303318	Protein FAM49B	10			
100	GLELQPQDNNGLCDPYIK	Non-raft	0.5	0.0	1.67	0	0	1	0	FER1L3	IPI00021048	Isoform 1 of Myoferlin	1574			
101	HSATTVFGANTPIVSCNFDR	Non-raft	0.5	0.0	1.67	0	0	1	0	FER1L3	IPI00021048	Isoform 1 of Myoferlin	1131			
102	IVGPSGAAPVCKVEPGLGADNSVVR	Non-raft	0.5	0.0	1.67	0	0	1	0	FLNA	IPI00302592	filamin 1	1018			
103	SPYTVTVGQACNPSACR	Non-raft	0.0	0.5	0.00	0	1	0	0	FLNA	IPI00302592	filamin 1	478			
104	SPYTVTVGQACNPSACR	Non-raft	0.0	0.5	0.00	0	1	0	0	FLNA	IPI00302592	filamin 1	483			
105	SPFVVQVGEACNPNACR	Non-raft	0.5	0.0	1.67	1	0	0	0	FLNB	IPI00477536	Filamin B	455			
106	SSTETCYSAIPK	Non-raft	0.5	0.0	1.67	1	0	0	0	FLNB	IPI00477536	Filamin B	2490			
107	EMLAAACQMFLGK	Raft	0.5	0.0	1.67	0	0	1	0	FLOT1	IPI00027438	Flotillin-1	85	12370178	34	Mouse
108	MFFTCTCPNEAMVVSGFRCR	Raft	1.0	0.0	3.33	1	0	1	0	FLOT1	IPI00027438	Flotillin-1	17			
109	VFVLPICIQIQR	Non-raft	1.5	0.0	5.00	1	0	2	0	FLOT1	IPI00027438	Flotillin-1	34			
		Raft	2.0	0.0	6.67	3	0	1	0	FLOT1	IPI00027438	Flotillin-1	34			
110	HVGSNLCLDSR	Non-raft	0.5	0.0	1.67	1	0	0	0	GALNT2	IPI00004669	Polypeptide N-acetylglactosaminyltransferase 2	496			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
111	IISNASCTTNCLAPLAK	Non-raft	4.5	1.0	4.50	5	1	4	1	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	152	16128592	244	Rabbit
		Raft	0.5	0.0	1.67	0	0	1	0	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	156			
112	IISNASCTTNCLAPLAK	Non-raft	3.5	3.0	1.17	4	4	3	2	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	156			
		Raft	1.0	0.5	2.00	1	1	1	0	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	160			
113	IISNASCTTNCLAPLAK	Non-raft	3.0	3.0	1.00	3	4	3	2	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	152/156			
		Raft	0.5	0.5	1.00	1	1	0	0	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	156/160			
114	VPTANVSVVDLTCR	Non-raft	3.0	2.0	1.50	3	1	3	3	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	247			
		Raft	0.5	0.0	1.67	1	0	0	0	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	247			
115	FCENTQAGEGR	Non-raft	0.5	0.0	1.67	1	0	0	0	GLG1	IPI00414717	golgi apparatus protein 1	324			
116	LSSDCEDQIR	Non-raft	0.5	0.0	1.67	1	0	0	0	GLG1	IPI00414717	golgi apparatus protein 1	542			
117	MACCKEDVLK	Non-raft	0.5	0.0	1.67	1	0	0	0	GLG1	IPI00414717	golgi apparatus protein 1	515			
118	FSPDLWGVSVCTVDGQR	Non-raft	0.0	0.5	0.00	0	1	0	0	GLS	IPI00215687	Isoform GAC of Glutaminase kidney isoform, mitochondrial precursor	266			
		Non-raft	0.0	0.5	0.00	0	1	0	0	GLS	IPI00289159	Isoform KGA of Glutaminase kidney isoform, mitochondrial precursor	266			
119	MFVDLNPDSKIIYSHFTCATDTENIR	Non-raft	0.5	0.0	1.67	1	0	0	0	GNA11	IPI00305551	Guanine nucleotide-binding protein subunit alpha-11	330	9175863	9/10	Human
		Non-raft	0.5	0.0	1.67	1	0	0	0	GNAQ	IPI00288947	Guanine nucleotide binding protein	330	8227063	9/10 (3/4)	Human
120	TLESMMACCLSDDEVK	Non-raft	1.5	0.0	5.00	2	0	1	0	GNA11	IPI00305551	Guanine nucleotide-binding protein subunit alpha-11	9/10			
121	EIYTHFTCATDTK	Raft	0.5	0.0	1.67	1	0	0	0	GNAI1	IPI00337415	Guanine nucleotide-binding protein G(i), alpha-1 subunit	325	8484716	3 (similarity)	Human
		Raft	0.5	0.0	1.67	1	0	0	0	GNAI2	IPI00748145	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	327	8484716	3 (similarity)	Human
		Raft	0.5	0.0	1.67	1	0	0	0	GNAI3	IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha	325			
122	LFDSICNNK	Non-raft	1.0	0.0	3.33	1	0	1	0	GNAI1	IPI00337415	Guanine nucleotide-binding protein G(i), alpha-1 subunit	254			
		Raft	0.5	0.0	1.67	1	0	0	0	GNAI1	IPI00337415	Guanine nucleotide-binding protein G(i), alpha-1 subunit	254			
		Non-raft	1.0	0.0	3.33	1	0	1	0	GNAI2	IPI00748145	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	255			
		Raft	0.5	0.0	1.67	1	0	0	0	GNAI2	IPI00748145	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	255			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
		Non-raft	1.0	0.0	3.33	1	0	1	0	GNAI3	IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha	254			
		Raft	0.5	0.0	1.67	1	0	0	0	GNAI3	IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha	254			
		Non-raft	0.5	0.0	1.67	1	0	0	0	GNAO1	IPI00220281	Guanine nucleotide-binding protein G(o) subunit alpha 1	255	8484716	3 (similarity)	Human
		Raft	0.5	0.0	1.67	1	0	0	0	GNAO1	IPI00220281	Guanine nucleotide-binding protein G(o) subunit alpha 1	255			
123	IIHEDGYSEEE <u>C</u> R	Non-raft	1.5	0.0	5.00	2	0	1	0	GNAI2	IPI00748145	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	66			
		Raft	0.5	0.0	1.67	1	0	0	0	GNAI2	IPI00748145	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	66			
124	LWADHGVQAC <u>F</u> GR	Non-raft	0.5	0.0	1.67	1	0	0	0	GNAI2	IPI00748145	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	140			
125	QLFALS <u>C</u> TAAEQGVLPDDLSGVIR	Non-raft	1.0	0.0	3.33	1	0	1	0	GNAI2	IPI00748145	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	112			
126	DGGVQAC <u>F</u> SR	Non-raft	0.5	0.0	1.67	0	0	1	0	GNAI3	IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha	139	8484716	3 (similarity)	Human
		Raft	0.5	0.0	1.67	1	0	0	0	GNAI3	IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha	139			
127	IIHEDGYSEDE <u>C</u> KQYK	Non-raft	1.5	0.0	5.00	2	0	1	0	GNAI3	IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha	66			
128	SPLT <u>I</u> CYPEYTGSENTYEEAAAY <u>I</u> QCQFEDLN R	Non-raft	0.5	0.0	1.67	1	0	0	0	GNAI3	IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha	305			
129	SLWNDPGIQE <u>C</u> YDR	Non-raft	1.0	0.0	3.33	1	0	1	0	GNAQ	IPI00288947	Guanine nucleotide binding protein	144			
130	TLESIMA <u>C</u> CLSEAK	Non-raft	0.5	0.0	1.67	0	0	1	0	GNAQ	IPI00288947	Guanine nucleotide binding protein	9/10			
131	HY <u>C</u> YPHFT <u>C</u> AVDTENIRR	Raft	0.5	0.0	1.67	1	0	0	0	GNAS	IPI00219835	Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	345	8484716	3 (similarity)	Human
		Raft	0.5	0.0	1.67	1	0	0	0	GNAS	IPI00514055	Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	359			
		Raft	0.5	0.0	1.67	1	0	0	0	GNAS	IPI00644936	Guanine nucleotide-binding protein G-s-alpha-3	344			
132	SNEYQLID <u>C</u> AQYFLDKIDVIK	Non-raft	1.0	0.0	3.33	2	0	0	0	GNAS	IPI00219835	Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	160			
		Raft	0.5	0.0	1.67	0	0	1	0	GNAS	IPI00219835	Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	160			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
		Non-raft	1.0	0.0	3.33	2	0	0	0	GNAS	IPI00514055	Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	174			
		Raft	0.5	0.0	1.67	0	0	1	0	GNAS	IPI00514055	Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	174			
		Non-raft	1.0	0.0	3.33	2	0	0	0	GNAS	IPI00514055	Isoform Gnas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	174			
		Raft	0.5	0.0	1.67	0	0	1	0	GNAS	IPI00644936	Guanine nucleotide-binding protein G-s-alpha-3	159			
133	A <u>C</u> ADATLSQITNNIDPVGR	Non-raft	0.5	0.5	1.00	1	1	0	0	GNB1	IPI00026268	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	25			
134	LFVSGA <u>C</u> DASAK	Non-raft	0.5	0.5	1.00	1	1	0	0	GNB1	IPI00026268	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	204			
135	FSPNSSNPIIVS <u>C</u> GWDK	Non-raft	0.5	0.0	1.67	0	0	1	0	GNB2L1	IPI00641950	Lung cancer oncogene 7	198			
136		Raft	1.5	0.5	3.00	1	1	2	0	GNB2L1	IPI00641950	Lung cancer oncogene 7	198			
137	LWNTLG <u>V</u> <u>C</u> K	Raft	0.5	1.0	0.50	1	1	0	1	GNB2L1	IPI00641950	Lung cancer oncogene 7	168			
138	TNHIGHTGYLNTVTVPDGS <u>I</u> CASGGK	Raft	1.0	0.5	2.00	2	1	0	0	GNB2L1	IPI00641950	Lung cancer oncogene 7	237			
139	VWNLAN <u>C</u> K	Raft	0.5	0.0	1.67	1	0	0	0	GNB2L1	IPI00641950	Lung cancer oncogene 7	212			
140	YWL <u>C</u> AATGPSIK	Non-raft	0.5	1.0	0.50	0	1	1	1	GNB2L1	IPI00641950	Lung cancer oncogene 7	279			
		Raft	1.0	0.5	2.00	0	1	2	0	GNB2L1	IPI00641950	Lung cancer oncogene 7	279			
141	NPMDYPVEDAF <u>C</u> KPQLVK	Raft	2.5	0.0	8.33	3	0	2	0	GPRC5A	IPI00022624	Retinoic acid-induced protein 3	284			
142	AYLEGT <u>C</u> VEWLR	Non-raft	2.5	0.5	5.00	1	1	4	0	HLA-A	IPI00743503	HLA class I histocompatibility antigen, A-34 alpha chain precursor	188			
		Raft	0.5	0.0	1.67	1	0	0	0	HLA-A	IPI00743503	HLA class I histocompatibility antigen, A-34 alpha chain precursor	188			
		Non-raft	2.5	0.5	5.00	1	1	4	0	HLA-C	IPI00473131	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	188	17785801	-	Human
		Raft	0.5	0.0	1.67	1	0	0	0	HLA-C	IPI00473131	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	188			
143	AYLEGL <u>C</u> VEWLR	Non-raft	2.5	0.5	5.00	1	1	4	0	HLA-B	IPI00471955	HLA class I histocompatibility antigen, B-50 alpha chain precursor	188	17785801	-	Human
		Raft	0.5	0.0	1.67	1	0	0	0	HLA-B	IPI00471955	HLA class I histocompatibility antigen, B-50 alpha chain precursor	188			
144	YT <u>C</u> HVQHEGLPKPLTLR	Non-raft	0.5	0.0	1.67	1	0	0	0	HLA-A	IPI00743503	HLA class I histocompatibility antigen, A-34 alpha chain precursor	283			
		Non-raft	0.5	0.0	1.67	1	0	0	0	HLA-B	IPI00471955	HLA class I histocompatibility antigen, B-50 alpha chain precursor	283			
145	MYG <u>C</u> DLGPDGR	Non-raft	2.5	0.0	8.33	2	0	3	0	HLA-B	IPI00471955	HLA class I histocompatibility antigen, B-50 alpha chain precursor	125			
		Non-raft	2.5	0.0	8.33	2	0	3	0	HLA-C	IPI00473131	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	125			
146	GG <u>S</u> CQAASSNSAQGSDES <u>L</u> I <u>C</u> K <u>A</u>	Non-raft	1.0	0.0	3.33	2	0	0	0	HLA-C	IPI00473131	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	345			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
147	VFNVFCLYGNVEK	Raft	0.5	0.5	1.00	1	1	0	0	HNRNPL	IPI00027834	heterogeneous nuclear ribonucleoprotein L isoform a	404			
148	TGEGFLCVFAINNTK	Non-raft	0.5	0.0	1.67	0	0	1	0	HRAS	IPI00000006	GTPase HRas precursor	80	10504264	181/184	Human
		Non-raft	0.5	0.0	1.67	0	0	1	0	KRAS	IPI00423568	Isoform 2A of GTPase KRas	80	3023817	180	Human
149	AAVEEGIVLGGCCALLR	Non-raft	0.0	1.0	0.00	0	1	0	1	HSPD1	IPI00472102	Heat shock protein 60	442			
150	DLEGTYLCCR	Non-raft	0.0	1.0	0.00	0	1	0	1	ICAM1	IPI00008494	Intercellular adhesion molecule 1 precursor	457			
151	YSDNWEAITGTGDPEHYLINVCK	Non-raft	0.5	0.0	1.67	0	0	1	0	IGF2R	IPI00289819	Cation-independent mannose-6-phosphate receptor precursor	586			
152	SETVLTCAATGR	Non-raft	1.0	0.0	3.33	2	0	0	0	ITGA3	IPI00215995	Isoform Alpha-3A of Integrin alpha-3 precursor	904			
153	TGAVYLCPLTAHK	Non-raft	0.5	0.5	1.00	1	1	0	0	ITGA3	IPI00215995	Isoform Alpha-3A of Integrin alpha-3 precursor	94			
154	CDDLEALK	Non-raft	0.5	0.0	1.67	1	0	0	0	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	64			
155	FCECDNFNCDR	Non-raft	1.5	0.5	3.00	2	1	1	0	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	555			
156	FCECDNFNCDR	Non-raft	0.5	0.5	1.00	0	0	1	1	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	560			
157	FCECDNFNCDR	Non-raft	0.0	0.5	0.00	0	1	0	0	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	553/555			
158	FCECDNFNCDR	Non-raft	0.0	0.5	0.00	0	1	0	0	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	553			
159	GCPPDDIENPR	Non-raft	0.5	2.0	0.25	1	4	0	0	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	75			
160	LPQPVQPDVPVSHCK	Non-raft	0.5	1.5	0.33	0	2	1	1	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	691			
161	SNGLICGGNGVCK	Non-raft	0.5	1.0	0.50	1	1	0	1	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	568			
162	SNGLICGGNGVCK	Non-raft	0.5	1.0	0.50	0	1	1	1	ITGB1	IPI00645194	integrin beta 1 isoform 1A precursor	574			
163	LVQNCCLWTLR	Non-raft	0.0	0.5	0.00	0	0	0	1	JUP	IPI00554711	Junction plakoglobin	372			
		Raft	0.0	0.5	0.00	0	0	0	1	JUP	IPI00554711	Junction plakoglobin	372			
164	NLALCPANHAPLQEAAVIPR	Raft	0.5	0.0	1.67	1	0	0	0	JUP	IPI00554711	Junction plakoglobin	511			
165	VLSVCPSNKPAIVEAGGMQALGK	Raft	0.0	0.5	0.00	0	1	0	0	JUP	IPI00554711	Junction plakoglobin	341			
166	VIGSGCNLDSAR	Non-raft	0.5	1.0	0.50	1	1	0	1	LDHA	IPI00217966	lactate dehydrogenase A	163			
		Non-raft	0.5	1.0	0.50	1	1	0	1	LDHB	IPI00219217	L-lactate dehydrogenase B chain	164			
167	ACGLVASNLNLKPGBCLR	Non-raft	2.0	0.5	4.00	2	0	2	1	LGALS1	IPI00219219	Galectin-1	3/17			
		Raft	2.0	1.0	2.00	2	2	2	0	LGALS1	IPI00219219	Galectin-1	3/17			
168	ACGLVASNLNLKPGBCLR	Non-raft	1.0	0.5	2.00	1	0	1	1	LGALS1	IPI00219219	Galectin-1	3			
		Raft	1.5	0.5	3.00	1	1	2	0	LGALS1	IPI00219219	Galectin-1	3			
169	ACGLVASNLNLKPGBCLR	Non-raft	2.0	0.0	6.67	2	0	2	0	LGALS1	IPI00219219	Galectin-1	17			
		Raft	2.0	1.0	2.00	2	2	2	0	LGALS1	IPI00219219	Galectin-1	17			
170	DSNNLCLHFNPR	Raft	0.0	0.5	0.00	0	1	0	0	LGALS1	IPI00219219	Galectin-1	43			
171	FNAHGDANTIVCNSK	Non-raft	1.0	0.5	2.00	1	1	1	0	LGALS1	IPI00219219	Galectin-1	61			
		Raft	1.0	0.5	2.00	2	1	0	0	LGALS1	IPI00219219	Galectin-1	61			
172	WTELAGCTADFR	Non-raft	0.5	0.0	1.67	1	0	0	0	LMAN2	IPI00009950	Vesicular integral-membrane protein VIP36 precursor	202			
173	AQNTWGCNLSLR	Raft	0.5	0.5	1.00	1	1	0	0	LMNA	IPI00021405	Isoform A of Lamin-A/C	522			
174	ISDYVGTCCER	Non-raft	0.5	0.0	1.67	1	0	0	0	LOC153364	IPI00293336	similar to metallo-beta-lactamase superfamily protein	212			
175	LVEALCAEHQINLIK	Raft	0.5	0.0	1.67	1	0	0	0	LOC440055	IPI00456898	PREDICTED: similar to ribosomal protein S12	70			
176	MFHCIPLWR	Non-raft	1.0	0.0	3.33	1	0	1	0	LRRC1	IPI00427739	Isoform 1 of Leucine-rich repeat-containing protein 1	4			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
177	CCC PEALYAAGK	Non-raft	0.5	0.0	1.67	1	0	0	0	LSR	IPI00409640	Isoform 1 of Lipolysis-stimulated lipoprotein receptor	302/303/304			
		Raft	0.5	0.0	1.67	1	0	0	0	LSR	IPI00409640	Isoform 1 of Lipolysis-stimulated lipoprotein receptor	302/303/304			
178	GMEQFPHLAFWQDLGNLVADGCDFV C R	Non-raft	0.5	0.0	1.67	1	0	0	0	M6PR	IPI00025049	Cation-dependent mannose-6-phosphate receptor precursor	240/244			
179	RAVVMIS C NR	Non-raft	0.5	0.0	1.67	0	0	1	0	M6PR	IPI00025049	Cation-dependent mannose-6-phosphate receptor precursor	145	8647889	34	Bovine
180	G C DVVVIPAGVPR	Non-raft	0.0	0.5	0.00	0	0	0	1	MDH2	IPI00291006	Malate dehydrogenase, mitochondrial precursor	93			
181	GYLGPQLPD C LK	Non-raft	0.5	0.0	1.67	1	0	0	0	MDH2	IPI00291006	Malate dehydrogenase, mitochondrial precursor	89			
182	THIPLISQ C TPK	Non-raft	0.5	0.0	1.67	1	0	0	0	MDH2	IPI00291006	Malate dehydrogenase, mitochondrial precursor	212			
183	RLLY C QR	Non-raft	0.5	0.0	1.67	1	0	0	0	MMP14	IPI00218398	Matrix metalloproteinase-14 precursor	574	15946988	574	Human
184	DWDNSGPF C GTISSK	Non-raft	1.0	0.0	3.33	1	0	1	0	MPP6	IPI00303280	MAGUK p55 subfamily member 6	298			
185	TCILDVNPQALK	Non-raft	0.5	0.0	1.67	1	0	0	0	MPP6	IPI00303280	MAGUK p55 subfamily member 6	432			
186	ALALAALAAVEPA C GSR	Non-raft	0.5	0.0	1.67	1	0	0	0	NDFIP1	IPI00012235	Isoform 1 of NEDD4 family-interacting protein 1	15			
187	GDF C IQVGR	Non-raft	0.5	0.0	1.67	0	0	1	0	NME1	IPI00012048	Nucleoside diphosphate kinase A	109			
188	GAEDGTSVQASES C LFR	Non-raft	0.5	0.0	1.67	0	0	1	0	NPC1	IPI00005107	Niemann-Pick C1 protein precursor	816			
189	IGFAPSSWIDDYFDWVKPQSS C CR	Non-raft	0.5	0.0	1.67	0	0	1	0	NPC1	IPI00005107	Niemann-Pick C1 protein precursor	956			
190	NRLDIF C CVR	Non-raft	0.5	0.0	1.67	1	0	0	0	NPC1	IPI00005107	Niemann-Pick C1 protein precursor	799/800			
191	TGEGFL C VFAINNSK	Non-raft	1.0	0.0	3.33	1	0	1	0	NRAS	IPI00000005	GTPase NRas precursor	80	2661017	181	Human
192	AADYNQALGT C R	Non-raft	0.5	0.0	1.67	1	0	0	0	NRSN2	IPI00017231	Protein C20orf98	115			
193	MGVVE C AK	Raft	0.5	0.0	1.67	1	0	0	0	PA2G4	IPI00299000	Proliferation-associated protein 2G4	296			
194	LVVPATQ C CGSLIGK	Non-raft	0.5	0.5	1.00	1	1	0	0	PCBP1	IPI00016610	Poly(rC)-binding protein 1	119			
195	VDCTANTNT C NK	Non-raft	0.0	0.5	0.00	0	1	0	0	PDIA3	IPI00025252	Protein disulfide-isomerase A3 precursor	92			
196	CGLA C ER	Raft	1.0	0.0	3.33	2	0	0	0	PERP	IPI00293189	Isoform 1 of p53 apoptosis effector related to PMP-22	8			
197	YADLTEDQLPSCESLKDTIAR	Non-raft	1.0	0.0	3.33	1	0	1	0	PGAM1	IPI00549725	Phosphoglycerate mutase 1	153			
198	AEGSDVANAVLDGAD C IMLSGETAKGDYP LEAVR	Non-raft	1.0	0.0	3.33	2	0	0	0	PKM2	IPI00479186	pyruvate kinase 3 isoform 1	358			
199	AGKPVICATQMLESNIK	Non-raft	0.0	0.5	0.00	0	1	0	0	PKM2	IPI00479186	pyruvate kinase 3 isoform 1	326			
200	GIFPVLCCKDPVQEAWAEDVDLR	Non-raft	1.0	0.0	3.33	1	0	1	0	PKM2	IPI00479186	pyruvate kinase 3 isoform 1	474			
201	NTGIICTIGPASR	Non-raft	2.0	1.5	1.33	2	1	2	2	PKM2	IPI00479186	pyruvate kinase 3 isoform 1	49			
202	LSAPGCWAACTNFNR	Non-raft	1.0	0.0	3.33	1	0	1	0	PLP2	IPI00030362	Proteolipid protein 2	12/16			
203	VYFAAEDTD C CTR	Non-raft	1.5	0.0	5.00	2	0	1	0	PLSCR1	IPI00005181	Phospholipid scramblase 1	148/149	12564925	184~189	Human
		Raft	0.5	0.0	1.67	1	0	0	0	PLSCR1	IPI00005181	Phospholipid scramblase 1	148/149			
204	SGAGQLPGQAAEESN C CAR	Non-raft	1.0	0.0	3.33	2	0	0	0	PLSCR3	IPI00216127	Phospholipid scramblase 3	125/126		211/214/216 (probable)	Human
205	SGAGQLPGQAAEESN C CAR	Non-raft	0.5	0.0	1.67	1	0	0	0	PLSCR3	IPI00216127	Phospholipid scramblase 3	126			
206	HTGPGILSMANAGPNTNGSQFF C TAK	Non-raft	0.5	0.0	1.67	1	0	0	0	PPIA	IPI00419585	Peptidyl-prolyl cis-trans isomerase A	115			
207	IIPGFMCQGGDFTR	Non-raft	1.0	0.0	3.33	1	0	1	0	PPIA	IPI00419585	Peptidyl-prolyl cis-trans isomerase A	62			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
		Raft	0.5	0.0	1.67	0	0	1	0	PPIA	IPI00419585	Peptidyl-prolyl cis-trans isomerase A	62			
208	KITIA D CGQLE	Raft	0.0	0.5	0.00	0	1	0	0	PPIA	IPI00419585	Peptidyl-prolyl cis-trans isomerase A	161			
209	LVQAFQFTDKHGE V CPAGWKPGSDTIKPDVQK	Raft	0.5	0.0	1.67	1	0	0	0	PRDX1	IPI00000874	Peroxiredoxin-1	173			
210	GKD C AVIVTQK	Non-raft	0.5	0.0	1.67	1	0	0	0	PSMA6	IPI00029623	Proteasome subunit alpha type 6	47			
211	A C LDYPVTSVLPPAS L CK	Non-raft	1.0	0.0	3.33	1	0	1	0	PTTG1IP	IPI00023974	Pituitary tumor-transforming gene 1 protein-interacting protein precursor	66/81			
		Raft	0.5	0.0	1.67	1	0	0	0	PTTG1IP	IPI00023974	Pituitary tumor-transforming gene 1 protein-interacting protein precursor	66			
212	NVS C LW C NTNK	Non-raft	0.5	0.0	1.67	1	0	0	0	PTTG1IP	IPI00023974	Pituitary tumor-transforming gene 1 protein-interacting protein precursor	57/60			
213	VTFSQDPTTVA L C ISK	Non-raft	0.5	0.0	1.67	1	0	0	0	PVRL2	IPI00022661	Isoform Delta of Poliovirus receptor-related protein 2 precursor	183			
214	LLLG N K C DMEAK	Non-raft	0.5	0.0	1.67	1	0	0	0	RAB13	IPI00016373	Ras-related protein Rab-13	123			
215	YLE C SALTQR	Non-raft	1.0	0.0	3.33	1	0	1	0	RAC1	IPI00010271	Isoform A of Ras-related C3 botulinum toxin substrate 1 precursor	157			
		Raft	0.5	0.5	1.00	1	1	0	0	RAC1	IPI00010271	Isoform A of Ras-related C3 botulinum toxin substrate 1 precursor	157			
216	QW N N C AFLESSAK	Non-raft	1.0	0.5	2.00	1	1	1	0	RAP1B	IPI00015148	Ras-related protein Rap-1b precursor	141			
217	ALAE E WG C PFMETS A K	Non-raft	0.5	0.0	1.67	0	0	1	0	RAP2A	IPI00019346	Ras-related protein Rap-2a	140			
		Raft	0.5	0.0	1.67	1	0	0	0	RAP2B	IPI00018364	Ras-related protein Rap-2b precursor	140	18582561	176/177	Human
218	ALAQEWG C PFMETS A K	Non-raft	1.5	0.0	5.00	1	0	2	0	RAP2C	IPI00009607	Ras-related protein Rap-2c precursor	140			
219	LYGSL P C VLLER	Non-raft	0.5	0.0	1.67	0	0	1	0	RCE1	IPI00031755	CAAX prenyl protease 2	85			
220	N C MTDLLAKLEAK	Non-raft	1.0	0.0	3.33	1	0	1	0	REEP5	IPI00024670	Receptor expression-enhancing protein 5	18			
221	C TTEAEQDIEEEKVEK	Raft	0.5	0.0	1.67	1	0	0	0	RELL1	IPI00216890	Similar to expressed sequence AA536743	88			
222	IGA F GYME C SAK	Non-raft	1.0	0.0	3.33	0	0	2	0	RHOA	IPI00027500	Transforming protein RhoA precursor	159			
223	HF C PNVPILVANKK	Non-raft	1.0	0.0	3.33	1	0	1	0	RHOB	IPI00000041	Rho-related GTP-binding protein RhoB precursor	107	1400319	189/192	Human
224	VL P C AHAYHSR	Non-raft	0.5	0.0	1.67	1	0	0	0	RNF167	IPI00023511	RING finger protein 167 precursor	248			
225	C TGGEVGATSALAPK	Non-raft	0.5	0.0	1.67	0	0	1	0	RPL12	IPI00024933	60S ribosomal protein L12	17			
		Raft	0.5	0.0	1.67	1	0	0	0	RPL12	IPI00024933	60S ribosomal protein L12	12			
226	LVILANN C PALR	Non-raft	0.5	0.0	1.67	0	0	1	0	RPL30	IPI00219156	60S ribosomal protein L30	52			
227	V C TLAIIDPGDSDIIR	Non-raft	0.5	0.0	1.67	0	0	1	0	RPL30	IPI00219156	60S ribosomal protein L30	92			
228	VGLTNYAAAY C TGLLLAR	Raft	1.5	0.5	3.00	1	1	2	0	RPL5	IPI00000494	60S ribosomal protein L5	100			
229	VTNRDI C QIAYAR	Raft	1.0	0.0	3.33	1	0	1	0	RPL5	IPI00000494	60S ribosomal protein L5	62			
230	C PFTGNVSIR	Non-raft	0.5	0.0	1.67	1	0	0	0	RPS11	IPI00025091	40S ribosomal protein S11	60			
231	LG E WVGL C CK	Raft	0.5	0.0	1.67	0	0	1	0	RPS12	IPI00013917	40S ribosomal protein S12	92			
232	G C TATLG N FAK	Raft	0.5	0.0	1.67	0	0	1	0	RPS2	IPI00013485	40S ribosomal protein S2	229			
233	GL C AIAQAESLR	Non-raft	0.5	0.0	1.67	1	0	0	0	RPS3	IPI00011253	40S ribosomal protein S3	97			
		Raft	1.0	0.5	2.00	1	1	1	0	RPS3	IPI00011253	40S ribosomal protein S3	97			
234	TIA E C LAD E LINA A K	Non-raft	1.0	0.5	2.00	1	0	1	1	RPS5	IPI00008433	40S ribosomal protein S5	172			
		Raft	1.0	0.5	2.00	0	0	2	1	RPS5	IPI00008433	40S ribosomal protein S5	172			
235	VNQAIW L C TGAR	Raft	1.5	0.0	5.00	2	0	1	0	RPS5	IPI00008433	40S ribosomal protein S5	155			
236	ADHQPLTEASYVNLPTIA I C NTDSPLR	Raft	1.0	0.5	2.00	1	1	1	0	RPSA	IPI00413108	Ribosomal protein SA	153			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
237	NTSAVLG C LAEK	Non-raft	1.0	0.0	3.33	1	0	1	0	RSPRY1	IPI00061267	Ring finger and SPRY domain containing 1	208			
		Raft	1.0	0.0	3.33	1	0	1	0	RSPRY1	IPI00061267	Ring finger and SPRY domain containing 1	208			
238	YSNSALGHVN C TIK	Non-raft	0.5	0.0	1.67	1	0	0	0	RTN4	IPI00021766	Isoform 1 of Reticulon-4	1101			
239	LLETE C PQYIR	Non-raft	1.5	1.5	1.00	1	1	2	2	S100A8	IPI00007047	Protein S100-A8	42			
240	QNNWPPLPSW C PVKP C FYQDFSTEIPADYQ R	Non-raft	0.5	0.0	1.67	1	0	0	0	SCAMP2	IPI00218850	Secretory carrier-associated membrane protein 2	127/132			
241	QNNWPPLPSF C PVQP C FFQDISMEIPQEFQK	Non-raft	0.5	0.0	1.67	1	0	0	0	SCAMP3	IPI00306382	Isoform 1 of Secretory carrier-associated membrane protein 3	142/147			
242	SQEK C YLFWSSSK	Non-raft	0.5	0.0	1.67	1	0	0	0	SCARB1	IPI00177968	Isoform 1 of Scavenger receptor class B member 1	470			
243	AITIANQTN C PLYITK	Non-raft	0.5	0.0	1.67	1	0	0	0	SDF2L1	IPI00106642	Dihydropyrimidinase-like 2	248			
244	VGSVLQEG C CGK	Non-raft	0.0	0.5	0.00	0	1	0	0	SDHA	IPI00305166	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	536			
245	SPAESAAAGLT C LP SVTR	Non-raft	0.5	0.0	1.67	0	0	1	0	SFT2D3	IPI00166444	Vesicle transport protein SFT2C	67			
246	AALEALGS C LNNK	Non-raft	0.5	0.0	1.67	1	0	0	0	SHMT2	IPI00002520	Serine hydroxymethyltransferase, mitochondrial precursor	91			
247	LGLQ C LP SDGVQNVNQ	Non-raft	0.5	0.0	1.67	0	0	1	0	SLC19A1	IPI00375452	Folate transporter 1	580			
248	GLAAAEP TANGGLALASIEDQGAAAGG Y CG SR	Non-raft	2.0	0.0	6.67	3	0	1	0	SLC1A5	IPI00019472	Neutral amino acid transporter B(0)	39			
249	S C TVLNVEGDALGAGLLQNYVDRTESR	Non-raft	1.5	0.0	5.00	2	0	1	0	SLC1A5	IPI00019472	Neutral amino acid transporter B(0)	467			
250	SSVTHLL C ASK	Non-raft	1.0	0.0	3.33	1	0	1	0	SLC38A2	IPI00410034	Putative 40-9-1 protein	403			
251	IGSSELQEF C PTILQLDSR	Non-raft	1.5	0.0	5.00	2	0	1	0	SLC39A14	IPI00014236	KIAA0062 protein	118			
252	LVSgyDSYGN C GQK	Non-raft	2.0	0.0	6.67	2	0	2	0	SLC44A1	IPI00221393	Isoform 1 of Choline transporter-like protein 1	69			
253	SVAL C VAA C PR	Non-raft	0.5	0.0	1.67	1		0		SLC44A1	IPI00221393	Isoform 1 of Choline transporter-like protein 1	117			
254	IFDDSP C PFTAK	Non-raft	0.5	0.0	1.67	1		0		SLC44A2	IPI00293074	Isoform 2 of Choline transporter-like protein 2	399			
255	LLSLLPLS C QK	Non-raft	0.5	0.0	1.67	1		0		SLC5A6	IPI00031822	Sodium-dependent multivitamin transporter	577			
256	C CGL C V C P C NR	Raft	0.5	0.0	1.67	1	0	0	0	SNAP23	IPI00010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	79/80/83/85/87	12551899	80/83/85/87	Human
257	TTWGDGGENSF C NVVSK	Non-raft	1.0	0.0	3.33	1	0	1	0	SNAP23	IPI00010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	112			
		Raft	0.5	0.0	1.67	1	0	0	0	SNAP23	IPI00010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	112			
258	LLQEIVDQ C MNR	Non-raft	0.5	0.0	1.67	1	0	0	0	SPTLC1	IPI00005745	Serine palmitoyltransferase 1	419			
259	GPGLFFILP C TDSFIK	Non-raft	1.0	0.0	3.33	1	0	1	0	STOM	IPI00219682	Erythrocyte band 7 integral membrane protein	87	10338112	30/87	Human
		Raft	1.0	0.0	3.33	2	0	0	0	STOM	IPI00219682	Erythrocyte band 7 integral membrane protein	87			
260	L C LISTFLEDGIR	Non-raft	1.0	0.0	3.33	0	0	2	0	SURF4	IPI00399142	Surfeit 4	32			
261	LFGNMEGD C PSDWKTDST C R	Non-raft	1.0	0.0	3.33	1	0	1	0	TFRC	IPI00022462	Transferrin receptor protein 1	363	2398066	62/67	Human

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
262	SEGTYCCGPVPVR	Non-raft	0.5	0.0	1.67	1	0	0	0	TGM2	IPI00294578	Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	370			
263	SEGTYCCGPVPVR	Non-raft	0.0	0.5	0.00	0	1	0	0	TGM2	IPI00294578	Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	370/371			
264	TVSYNGILGPECGTK	Non-raft	0.0	0.5	0.00	0	1	0	0	TGM2	IPI00294578	Isoform 1 of Protein-glutamine gamma-glutamyltransferase 2	524			
265	SQGVFQCGPASVIGVR	Non-raft	0.0	1.0	0.00	0	2	0	0	TGM3	IPI00300376	Protein-glutamine gamma-glutamyltransferase E precursor	367			
		Raft	0.0	0.5	0.00	0	1	0	0	TGM3	IPI00300376	Protein-glutamine gamma-glutamyltransferase E precursor	367			
266	VLTAAGNSCR	Raft	0.5	0.0	1.67	1	0	0	0	THOC6	IPI00301252	Isoform 3 of THO complex subunit 6 homolog	279			
267	CSECIDWGEKR	Raft	1.0	0.0	3.33	2	0	0	0	TMEM50A	IPI00000612	Transmembrane protein 50A	10/13			
268	DNGFCSWLTAIFR	Non-raft	0.5	0.0	1.67	0	0	1	0	TMEM63B	IPI00514538	transmembrane protein 63B	126			
		Raft	0.5	0.0	1.67	1	0	0	0	TMEM63B	IPI00514538	transmembrane protein 63B	126			
269	NTACQCKPGTFR	Non-raft	1.0	0.0	3.33	2	0	0	0	TNFRSF10A	IPI00021975	Tumor necrosis factor receptor superfamily member 10A precursor	188/190			
270	NTACQCKPGTFR	Non-raft	0.5	0.0	1.67	1	0	0	0	TNFRSF10A	IPI00021975	Tumor necrosis factor receptor superfamily member 10A precursor	188			
271	YGQDYSTHWNDLLFCLR	Non-raft	0.5	0.0	1.67	1	0	0	0	TNFRSF10B	IPI00296379	Isoform Long of Tumor necrosis factor receptor superfamily member 10B precursor	113			
272	LLEQAEAEQCQR	Non-raft	0.5	0.0	1.67	1	0	0	0	TNFRSF10D	IPI00294516	Tumor necrosis factor receptor superfamily member 10D precursor	326			
273	VFLDNNPWVCDCHMADMVTWLK	Non-raft	0.5	0.0	1.67	1	0	0	0	TPBG	IPI00009111	Trophoblast glycoprotein precursor	298/300			
274	IAVAAQN ^C YK	Non-raft	0.0	0.5	0.00	0	1	0	0	TPI1	IPI00465028	Triosephosphate isomerase 1 variant	104			
275	IYGGSVTGATCK	Non-raft	1.0	0.5	2.00	1	1	1	0	TPI1	IPI00465028	Triosephosphate isomerase 1 variant	255			
276	VVNTQCGYDVR	Non-raft	0.5	0.0	1.67	0	0	1	0	TSPAN14	IPI00165394	Isoform 2 of Tetraspanin-14	183			
277	AVCMLSNTTAIAEAWAR	Non-raft	0.0	0.5	0.00	0	0	0	1	TUBA1A	IPI00180675	Tubulin alpha-3 chain	376	9247644	20/213/376	Porcine
		Non-raft	0.0	0.5	0.00	0	0	0	1	TUBA1B	IPI00387144	Tubulin alpha-ubiquitous chain	376			
		Non-raft	0.0	0.5	0.00	0	0	0	1	TUBA8	IPI00646909	Tubulin alpha-8 chain	376			
278	TIQFVDWCPTGFK	Non-raft	0.0	0.5	0.00	0	1	0	0	TUBA1A	IPI00180675	Tubulin alpha-3 chain	347			
		Non-raft	0.0	0.5	0.00	0	1	0	0	TUBA1C	IPI00218343	Tubulin alpha-6 chain	347			
		Non-raft	0.0	0.5	0.00	0	1	0	0	TUBA8	IPI00646909	Tubulin alpha-8 chain	347			
279	YMACCLLYR	Non-raft	0.5	0.0	1.67	1	0	0	0	TUBA1A	IPI00180675	Tubulin alpha-3 chain	316			
		Non-raft	0.5	0.0	1.67	1	0	0	0	TUBA1B	IPI00387144	Tubulin alpha-ubiquitous chain	316			
		Non-raft	0.5	0.0	1.67	1	0	0	0	TUBA1C	IPI00218343	Tubulin alpha-6 chain	316			
		Non-raft	0.5	0.0	1.67	1	0	0	0	TUBA4A	IPI00007750	Tubulin alpha-1 chain	316			
280	SIQFVDWCPTGFK	Non-raft	0.5	1.0	0.50	1	1	0	1	TUBA1B	IPI00387144	Tubulin alpha-ubiquitous chain	347			
		Raft	0.0	0.5	0.00	0	1	0	0	TUBA1B	IPI00387144	Tubulin alpha-ubiquitous chain	347			
		Non-raft	0.5	0.5	1.00	1	1	0	0	TUBA4A	IPI00007750	Tubulin alpha-1 chain	347			
281	TAVCDIPPR	Non-raft	0.0	0.5	0.00	0	0	0	1	TUBB	IPI00011654	Tubulin beta-2 chain	354			
		Non-raft	0.0	0.5	0.00	0	0	0	1	TUBB2A	IPI00013475	tubulin, beta 2	354			
		Non-raft	0.0	0.5	0.00	0	0	0	1	TUBB2C	IPI00007752	Tubulin beta-2C chain	354			
282	FIITALPTIYHCK	Non-raft	0.5	0.0	1.67	0	0	1	0	TXNDC1	IPI00395887	Thioredoxin domain-containing protein 1 precursor	116			

No.	Sequence	Fraction	Spectral Counts							Gene Symbol	Acc.Number	Description	Site	Reference	Known Sites	Organism
			Ave. EXP	Ave. CON	Ave. Ratio	1st EXP	1st CON	2nd EXP	2nd CON							
283	WGLGGT C VNVG C IPK	Non-raft	1.0	0.0	3.33	1	0	1	0	TXNRD1	IPI00554786	Thioredoxin reductase 1, cytoplasmic precursor	64			
		Non-raft	1.0	0.0	3.33	1	0	1	0	TXNRD2	IPI00157820	Isoform 2 of Thioredoxin reductase 2, mitochondrial precursor	91			
284	FSAVAL C K	Non-raft	0.5	0.0	1.67	1	0	0	0	UCHL1	IPI00018352	Ubiquitin carboxyl-terminal hydrolase isozyme L1	220			
285	QTIGNS C GTIGLIHAVANNQDKLGFEDGSVLK	Non-raft	0.5	0.0	1.67	0	0	1	0	UCHL1	IPI00018352	Ubiquitin carboxyl-terminal hydrolase isozyme L1	90			
286	A C GLNFADLMAR	Non-raft	0.0	0.5	0.00	0	1	0	0	VAT1	IPI00156689	Synaptic vesicle membrane protein VAT-1 homolog	86			
287	AIANE C QANFISIK	Non-raft	0.5	0.5	1.00	1	0	0	1	VCP	IPI00022774	Transitional endoplasmic reticulum ATPase	535			
288	GVLFGPPG C GK	Non-raft	0.5	0.0	1.67	1	0	0	0	VCP	IPI00022774	Transitional endoplasmic reticulum ATPase	522			
289	LGDVISIQ C PDVK	Non-raft	1.0	1.0	1.00	1	1	1	1	VCP	IPI00022774	Transitional endoplasmic reticulum ATPase	105			
290	QAAP C VLFDFDELDSIAK	Non-raft	0.5	0.5	1.00	1	1	0	0	VCP	IPI00022774	Transitional endoplasmic reticulum ATPase	572			
291	YQIDPD A C F SAK	Non-raft	0.5	0.5	1.00	1	1	0	0	VDAC1	IPI00216308	Voltage-dependent anion-selective channel protein 1	232			
292	ATHGQT C ARPM C IPPSYADLGK	Non-raft	0.5	0.0	1.67	1	0	0	0	VDAC2	IPI00216026	Isoform 1 of Voltage-dependent anion-selective channel protein 2	8/13			
293	ATHGQT C ARPM C IPPSYADLGK	Non-raft	0.5	0.5	1.00	1	1	0	0	VDAC2	IPI00216026	Isoform 1 of Voltage-dependent anion-selective channel protein 2	8			
294	QVQSLT C EVDAKGTNESLER	Raft	0.5	0.0	1.67	1	0	0	0	VIM	IPI00418471	Vimentin	328			
295	AANILVGENL V CK	Non-raft	0.5	0.0	1.67	0	0	1	0	YES1	IPI00013981	Proto-oncogene tyrosine-protein kinase Yes	410	7980442	3 (probable)	Monkey
		Raft	0.5	0.0	1.67	0	0	1	0	YES1	IPI00013981	Proto-oncogene tyrosine-protein kinase Yes	410			
296	GGVNPFTNG C CNNVSR	Non-raft	0.5	0.0	1.67	1	0	0	0	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	236/237			
297	VL C SSPAPR	Non-raft	0.5	0.0	1.67	1	0	0	0	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	245			
298	TFFTSP C TEEPR	Non-raft	1.0	0.0	3.33	2	0	0	0	ZDHHC6	IPI00008350	Isoform 1 of Probable palmitoyltransferase ZDHHC6	343			

Note 1. No. = Number (see the 1st column).

Note 2. Avg. = Average (see the 4th~6th columns)

Note 3. Acc. Number = Accession Number (see the 12th column)

Note 4. To avoid division by zero, a value of 0.3 was substituted for CON spectral counts of 0 (see the 5th column) so that the average EXP/CON ratios (see the 6th column) could be calculated.

Note 5. The peptide sequences (see the 2nd column) were assorted according to Gene Symbols (see the 11th column).

Note 6. The peptide sequences are only representative, since a maximum of one miscleavage may give rise to a maximum of 3 unique peptides.

Note 7. Cysteins in blue (bold and underlined, see the 2nd column) were carbamidomethylated, indicating they were originally S-acylated. Cysteines in red were modified by N-ethylmaleimide, indicating they were originally nonacylated.

Table S5. Localization of S-acylation sites using the peptide-based procedure.

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																		Gene Symbol	Acc.Number	Description	Site			
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate						2nd Biological Replicate						Avg. EXP	Avg. CON	Avg. Ratio							
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate										2nd Tech. Replicate		
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio								4th EXP	4th CON	4th Ratio
1	MLITSQAMDILRCNPQK	+	495.50	4	47.0	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	-	IPI00022913	PRO1575	13			
			495.55	4	48.7	Raft	+	0.50	0.25	2.00	1	0	6.67	0	1	0.00	0.5	0.5	1.00	0	0	0.00	1	0	6.67	-	IPI00022913	PRO1575				
2	TLACAGLDVCCGSEAGDAGTAGSSAR	-	650.45	4	47.0	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	-	IPI00024270	Hypothetical protein				
3	ADDLDFETGDAGASATFFMQCSALRK	-	920.71	3	81.0	Non-raft	-	0.50	0.50	1.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	2	0	13.33	0	1	0.00	-	IPI00218084	PREDICTED: similar to eukaryotic translation initiation factor 5A				
			920.61	3	92.3	Raft	+	1.25	0.75	1.67	1	1	1.00	1	2	0.50	1.0	1.5	0.67	1	0	6.67	2	0	13.33	-	IPI00218084	PREDICTED: similar to eukaryotic translation initiation factor 5A				
4	WEPGMVGAASSAAGESVCVQGCGR	-	599.71	4	44.3	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	-	IPI00295844	OTTHUMP0000031441				
5	AALEPFQTEEDSISVSDAPGSCIDCNENTR	+	1105.20	3	55.7	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	-	IPI00429529	HERV-K_12q14.1 provirus ancestral Gag polyprotein	111/115			
6	FISEPSTYVPAGSSATAWLRLCOAR	-	697.14	4	55.5	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	-	IPI00447734	Em:AC008101.5 protein				
7	GGRPGESSGR	+	355.21	3	46.8	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	-	IPI00514009	Novel protein	213			
8	SEDAPKIHMAISLSLFLNLTFLINVGSSSQGPASCVWR	-	1076.36	4	44.2	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	-	IPI00552637	G-protein coupled receptor				
9	NVLQLLCGRMK	-	359.32	4	46.5	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	-	IPI00644570	18 kDa protein				
10	LSATIASGYCGSDAMCLVR	-	682.02	3	44.8	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	-	IPI00646048	Novel protein				
11	LVIAADPGARVGSSCLGISAGIHLGEATGR	-	974.39	3	48.4	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	-	IPI00737515	PREDICTED: similar to Unc4.1 homeobox				
12	LGPSPGCPGSPVAGTVHHGPAQRPLAR	-	631.33	4	49.6	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	-	IPI00737760	PREDICTED: similar to BAH domain and coiled-coil containing 1				
13	KCLLLCQLR	+++	601.61	2	61.0	Non-raft	+++	0.75	0.00	5.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	1	0	6.67	1	0	6.67	-	IPI00747966	Conserved hypothetical protein	87/92			
			601.63	2	65.5	Raft	+++	0.75	0.00	5.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	1	0	6.67	1	0	6.67	-	IPI00747966	Conserved hypothetical protein				
14	ASHQAGLCSSQGRPEGCGDR	+	550.32	4	47.2	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	-	IPI00748363	Similar to UDP-glucuronate decarboxylase	96			
15	HLNLGHPVCLTSK	-	355.33	4	55.6	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	-	IPI00748374	Similar to Ras suppressor protein 1				
16	LRISSSLLHCSSSSDTLDR	-	722.44	3	56.3	Non-raft	-	0.00	0.75	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	2	0.00	-	IPI00749362	CDNA FLJ38877 fis, clone MESAN2015277				
			722.30	3	50.7	Raft	+	0.50	0.25	2.00	1	0	6.67	1	1	1.00	1.0	0.5	2.00	0	0	0.00	0	0	0.00	-	IPI00749362	CDNA FLJ38877 fis, clone MESAN2015277				
17	MPSFHVLAQCGLGPRNPLLGVEALFMTCPSSLLR	-	907.53	4	44.1	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	AAAS	IPI00792062	7 kDa protein				
18	CAAAGSSSSGSAALADADCLRK	+	552.84	4	46.2	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	ABHD12	IPI00060569	Isoform 2 of Abhydrolase domain-containing protein 12	34			
19	PQAAPCLSGAPQASAADVVVVHGR	-	576.66	4	54.6	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	ACAA1	IPI00011522	Homo sapiens clone 23623				
			576.63	4	48.9	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	ACAA1	IPI00011522	Homo sapiens clone 23623				
20	GVAALCIGGGMIAMCVQR	+	456.89	4	47.7	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	ACAT2	IPI00291419	Acetyl-coA acetyltransferase, cytosolic	383/393			
21	TGATRGAQEPQSVWPEPK	-	479.31	4	45.8	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	ACD	IPI00254484	Isoform 1 of Adrenocortical dysplasia protein homolog				
22	FRCPETLFPQSFIGMESAGIHETTYNSIMK	-	1146.05	3	46.6	Non-raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	ACTA1	IPI00021428	Actin, alpha skeletal muscle				
23	FRCPEALFPQSLFMESCGIHETTFNSIMK	++++	1183.39	3	115.6	Non-raft	++++	1.50	0.00	10.00	3	0	20.00	1	0	6.67	2.0	0.0	13.33	2	0	13.33	0	0	0.00	ACTB	IPI00021439	Actin, cytoplasmic 1	272			
																									ACTG1	IPI00021440	Actin, cytoplasmic 2	272				
			1183.33	3	114.6	Raft	++++	3.25	0.00	21.67	6	0	40.00	5	0	33.33	5.5	0.0	36.67	1	0	6.67	1	0	6.67	ACTB	IPI00021439	Actin, cytoplasmic 1				
																									ACTG1	IPI00021440	Actin, cytoplasmic 2					
24	LCYVALDFEQEMATAASSSSLEK	-	832.52	3	51.3	Raft	-	0.25	0.25	1.00	0	0	0.00	1	1	1.00	0.5	0.5	1.00	0	0	0.00	0	0	0.00	ACTB	IPI00021439	Actin, cytoplasmic 1				
																									ACTG1	IPI00021440	Actin, cytoplasmic 2					
25	DDIAALVVDNGSGMCK	-	883.41	2	137.8	Non-raft	-	6.00	8.50	0.71	6	8	0.75	6	8	0.75	6.0	8.0	0.75	5	10	0.50	7	8	0.88	ACTB	IPI00021439	Actin, cytoplasmic 1				
			883.59	2	145.9	Raft	-	14.00	12.00	1.17	16	17	0.94	14	13	1.08	15.0	15.0	1.00	14	10	1.40	12	8	1.50	ACTB	IPI00021439	Actin, cytoplasmic 1				
26	EEIEAALVIDNGSGMCK	-	911.15	2	114.8	Non-raft	-	3.75	8.25	0.45	4	7	0.57	1	7	0.14	2.5	7.0	0.36	5	11	0.45	5	8	0.63	ACTG1	IPI00021440	Actin, cytoplasmic 2				
			919.04	2	144.7	Raft	-	15.50	13.50	1.15	17	15	1.13	17	16	1.06	17.0	15.5	1.10	14	15	0.93	14	8	1.75	ACTG1	IPI00021440	Actin, cytoplasmic 2				
27	ELPDPQAEYCIAR	-	752.86	2	47.6	Non-raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	ACTN4	IPI00013808	Alpha-actinin-4				
			753.09	2	63.3	Raft	+	3.00	2.00	1.50	3	4	0.75	5	4	1.25	4.0	4.0	1.00	2	0	13.33	2	0	13.33	ACTN4	IPI00013808	Alpha-actinin-4				
28	CQLEINFNTLQTK	++	776.70	2	97.1	Raft	++	0.50	0.00	3.33	0	0	0.00	2	0	13.33	1.0	0.0	6.67	0	0	0.00	0	0	0.00	ACTN4	IPI00013808	Alpha-actinin-4	351			
29	AGRLPACVVDCTGTGYTK	-	939.77	2	56.5	Non-raft																										

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																				Gene Symbol	Acc.Number	Description	Site		
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate									2nd Biological Replicate													
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio					
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio								
			870.72	3	66.1	Raft	+++	0.75	0.00	5.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	AHNAK	IPI00555610	313 kDa protein		
37	MEVLGHFGQGSNGYLEALPSARGVSV ^{CL} R	+	1060.16	3	47.0	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	AKAP13	IPI00386928	CDNA FLJ11952 fis, clone HEMBB1000831, weakly similar to Homo sapiens breast cancer nuclear receptor-binding auxiliary protein (BRX) mRNA	28	
38	FMNSGQT ^C VAPDYIL ^C DPSIQNIVEKLK	-	1086.69	3	43.7	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ALDH3A1	IPI00296183	Aldehyde dehydrogenase, dimeric NADP-prefering		
39	YASIC ^C QQGIVPIVEPEILPDGDHDLK	+	989.32	3	48.8	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ALDOC	IPI00418262	Fructose-bisphosphate aldolase C	178	
40	YYHVFREGELEGA ^C R	-	611.04	3	47.3	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ALKBH8	IPI00154533	IMP dehydrogenase/GMP reductase family protein		
41	MAKMSPSG ^C CESSAGNR	-	407.04	4	45.4	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ALOX12	IPI00782956	22 kDa protein		
42	QNIDVFAQDM ^C GRDAEDYAISHHLTK	+	993.35	3	46.4	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ANKRD20A1	IPI00020265	Ankyrin repeat domain-containing protein 20A1	231	
43	SSSKPSC ^C SLASGLK	+	451.41	3	46.1	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ANKRD34C	IPI00741635	PREDICTED: similar to cytosolic phosphoprotein DP58 isoform 2	485	
44	AQQAASST ^C GQPPPATGSEQTGPHIR	+	669.96	4	52.2	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ANKRD6	IPI00032135	Isoform 1 of Ankyrin repeat domain-containing protein 6	607	
45	^C SDNTEVEVSNLENKQPVESTSAK	+	870.30	3	44.8	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ANLN	IPI00032958	Isoform 2 of Actin-binding protein anillin	71	
46	^S CEGQNPPELLPK	+++	657.95	2	56.0	Raft	+++	0.75	0.00	5.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ANLN	IPI00032958	Isoform 2 of Actin-binding protein anillin	309	
47	MFCGDYVQGTIFPAPNFNPIMDAQMLGGA LQGFD ^C CDK	+	1050.34	4	48.0	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ANXA10	IPI00296528	Annexin A10	35	
48	GLGTDEDSLIEI ^C CSR	-	861.05	2	72.4	Non-raft	-	0.25	0.75	0.33	0	1	0.00	1	2	0.50	0.5	1.5	0.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ANXA2P2	IPI00334627	Similar to annexin A2 isoform 1		
			861.21	2	72.3	Raft	-	0.25	1.25	0.20	0	2	0.00	0	2	0.00	0.0	2.0	0.00	1	0	6.67	0	1	0.00	0.5	0.5	1.00	ANXA2P2	IPI00334627	Similar to annexin A2 isoform 1		
49	STVHEIL ^C KLSELDHSTPPSAYGSVK	-	967.26	3	104.9	Non-raft	-	3.50	3.75	0.93	2	3	0.67	5	4	1.25	3.5	3.5	1.00	4	5	0.80	3	3	1.00	3.5	4.0	0.88	ANXA2P2	IPI00334627	Similar to annexin A2 isoform 1		
			966.81	3	111.0	Raft	+	4.75	2.25	2.11	4	2	2.00	5	4	1.25	4.5	3.0	1.50	6	1	6.00	4	2	2.00	5.0	1.5	3.33	ANXA2P2	IPI00334627	Similar to annexin A2 isoform 1		
50	M ^C FSAATDLGRGAVGNVSVLGR	-	564.28	4	52.3	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	AP3S1	IPI00014624	Adapter-related protein complex 3 sigma 1 subunit		
51	MSATW ^C SPPEGQMGQGPGREVGNSAAS GPASPIR	+	1150.41	3	47.1	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	APLN	IPI00419611	Apelin, AGTRL1 ligand	6	
52	CCALGRGTAWAAC ^C PGGACGLMEADPSPP HCQQQGK	-	1027.27	4	45.1	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ARHGAP27	IPI00795597	7 kDa protein		
53	GCGAFC ^C HDD ^C IGPSKLCVSC ^C LVVR	-	684.25	4	46.0	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	ASXL2	IPI00384569	Hypothetical protein KIAA1685		
54	MD ^C SLVR	++	433.33	2	57.4	Non-raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	2	0	13.33	1.0	0.0	6.67	ATP11A	IPI00255653	Probable phospholipid-transporting ATPase IH	3	
55	Y ^C AGEENWVDSR	++++	678.99	2	62.6	Non-raft	++++	2.50	0.00	16.67	3	0	20.00	2	0	13.33	2.5	0.0	16.67	3	0	20.00	2	0	13.33	2.5	0.0	16.67	ATP11A	IPI00255653	Probable phospholipid-transporting ATPase IH	14	
			715.10	2	84.6	Raft	+++	1.00	0.00	6.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ATP11A	IPI00255653	Probable phospholipid-transporting ATPase IH		
56	AAAAVGNVAP ^C CGARPC ^C GVRPDGQPKPGP QPR	+	1078.46	3	45.1	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ATP13A1	IPI00034277	Isoform A of Probable cation-transporting ATPase 13A1	18	
57	IISANGC ^C KVDNSSLTGESEPQTR	-	803.03	3	75.9	Non-raft	-	2.25	1.75	1.29	2	1	2.00	4	2	2.00	3.0	1.5	2.00	2	2	1.00	1	2	0.50	1.5	2.0	0.75	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor		
			803.03	3	85.0	Raft	+	1.75	0.75	2.33	1	2	0.50	2	1	2.00	1.5	1.5	1.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor		
58	LIIVEG ^C QOR	++	515.61	2	52.8	Non-raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	705	
59	NIAFSTNC ^C VEGTAR	+	815.66	2	87.1	Non-raft	+	1.75	0.75	2.33	2	1	2.00	2	2	1.00	2.0	1.5	1.33	2	0	13.33	1	0	6.67	1.5	0.0	10.00	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	249	
60	NLEAVETLGSTSTI ^C CDKGTGLTQNR	++++	914.46	3	64.9	Non-raft	++++	1.25	0.00	8.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	374	
																												ATP1A2	IPI00003021	Sodium/potassium-transporting ATPase alpha-1 chain precursor	372		
			914.43	3	52.9	Raft	++	0.50	0.00	3.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	1	0	6.67	0.5	0.0	3.33	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor		
																												ATP1A2	IPI00003021	Sodium/potassium-transporting ATPase alpha-2 chain precursor			
61	NKILIFGLLEETALAAFLSY ^C CPMGVVALR	+	1038.65	3	46.9	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	ATP1A2	IPI00003021	Sodium/potassium-transporting ATPase alpha-2 chain precursor	958	
62	GAPESVIER ^C SSVR	-	373.15	4	47.8	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	ATP2A3	IPI00004092	Isoform SERCA3B of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3		

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																				Gene Symbol	Acc.Number	Description	Site	
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate									2nd Biological Replicate												
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON					Avg. Ratio
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
63	ILAAQ ^C CKVDNSSLTGESEPQTR	–	802.78	3	104.8	Non-raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ATP4A	IP100218919	Potassium-transporting ATPase alpha chain 1	
64	AG ^C CEWLR	++	469.63	2	58.1	Non-raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ATP9A	IP100024368	Isoform Long of Probable phospholipid-transporting ATPase IIA	24/25
65	LRSPPPA ^C ASGAGPAGGVSLLLPR	+	561.89	4	53.2	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	B3GALNT2	IP100744286	Isoform 2 of UDP-GalNAc:beta-1,3-N-acetylgalactosaminyltransferase 2	30
66	SVEDVRPHHTDANNQSA ^C FEAPDQK	+	932.77	3	53.4	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	BAT2D1	IP100083708	HBxAg transactivated protein 2	897
67	LNVFAKPEATEVSPNKGTL SVMEDSAQEIA ^T CNSR	–	1247.33	3	71.5	Non-raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	BCAM	IP100002406	Lutheran blood group glycoprotein precursor	
68	SSEHINETGETAMLV ^{CK}	–	874.64	2	78.7	Non-raft	–	1.75	1.25	1.40	2	2	1.00	2	2	1.00	2.0	2.0	1.00	1	0	6.67	2	1	2.00	1.5	0.5	3.00	BSG	IP100019906	Isoform 2 of Basigin precursor	
			874.67	2	67.0	Raft	–	0.50	0.75	0.67	1	0	6.67	1	1	1.00	1.0	0.5	2.00	0	2	0.00	0	0	0.00	0.0	1.0	0.00	BSG	IP100019906	Isoform 2 of Basigin precursor	
69	SAASSVSFSPGGGGGGGAAAAAA ^{AC} R	+	550.13	4	50.0	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	C11orf61	IP100439946	c11orf61 protein	99
70	ML ^C TAA ^{YR} SLPFYIK	+	449.60	4	48.6	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	C12orf65	IP100794143	Hypothetical short protein	15
71	ATS ^{VL} ^C CLR	++++	504.58	2	78.8	Non-raft	++++	2.25	0.00	15.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	2	0	13.33	3	0	20.00	2.5	0.0	16.67	C13orf1	IP100030959	24 kDa protein	7/8
			504.35	2	69.5	Raft	+++	0.75	0.00	5.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	C13orf1	IP100030959	24 kDa protein	
72	SRFPY ^{CV} VWTP ^{IP} VLWFF ^{PI} IIGHM ^G CT ^S TGVIR	+	1000.07	4	45.1	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	C1orf160	IP100030236	Isoform 1 of Uncharacterized protein C1orf160	55
73	IDL ^C LSSEGSEVILATSSDEK	–	549.98	4	45.4	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	C1orf41	IP100098827	Placental protein 25	
74	ALVLD ^C HYPEDEVGQEDEAESDIFSIR	–	1027.36	3	48.6	Non-raft	–	0.00	0.50	0.00	0	1	0.00	0	1	0.00	0.0	1.0	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	C1QBP	IP100014230	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor	
75	CQAGLGS ^{GP} VSSSGR	–	444.84	3	63.5	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	C20orf181	IP100098823	Tissue plasminogen activator (Fragment)	
76	TLIKEIQSP ^{LS} SCDGSIALDAEPTVQ ^P PASLPR	+	1151.36	3	45.5	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	C2orf44	IP100018786	CDNA: FLJ121945 fis, clone HEP04702	507
77	VVS ^{VL} PRALS ^C VP ^{PH} LHR	+	728.33	3	50.0	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	C5orf34	IP100374273	CDNA FLJ32363 fis, clone PUAEN1000081	304
78	VQAQAFREGENTQVAEPE ^{AC} QDMYESLAR	++	1048.57	3	50.1	Non-raft	++	0.50	0.00	3.33	0	0	0.00	2	0	13.33	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	C6orf125	IP100031617	Protein C6orf125	53
79	RTFFN ^{IQ} ^C FMLTH	–	575.06	3	47.3	Raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	C7orf34	IP100064738	Isoform 1 of Protein c7orf34 precursor	
80	AGIF ^C LLEMAGGQASVVIIGSAGVLC ^R	+	1048.57	3	50.1	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CAMK2G	IP100555954	Calcium/calmodulin-dependent protein kinase II gamma isoform 6 variant (Fragment)	5
81	MFS ^C VKPYEDQ ^{NY} SALRR	++++	750.85	3	47.5	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	CAPN5	IP100643994	CDNA FLJ46245 fis, clone TEST14020596, highly similar to Homo sapiens calpain 5	44
			750.93	3	76.3	Raft	++++	1.75	0.00	11.67	3	0	20.00	2	0	13.33	2.5	0.0	16.67	2	0	13.33	0	0	0.00	1.0	0.0	6.67	CAPN5	IP100643994	CDNA FLJ46245 fis, clone TEST14020596, highly similar to Homo sapiens calpain 5	
82	C ^{FS} SVSLQ ^{LS} QSD	++++	658.01	2	77.5	Raft	++++	1.75	0.00	11.67	2	0	13.33	1	0	6.67	1.5	0.0	10.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	CAV2	IP100019870	Isoform Alpha of Caveolin-2	151
83	SVTD ^{VI} APL ^C TSVGR	+	815.73	2	45.5	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CAV2	IP100019870	Isoform Alpha of Caveolin-2	145
			816.14	2	53.6	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CAV2	IP100019870	Isoform Alpha of Caveolin-2	
84	ANCFSPVSGDK ^P CCR	++	919.70	2	73.8	Non-raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CD38	IP100006071	Isoform 1 of ADP-ribosyl cyclase 1	15/16
85	MPEEGSG ^C SVR	+	576.55	2	63.6	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	CD70	IP100031713	Tumor necrosis factor ligand superfamily member 7	8
86	CNPGFSS ^{FE} IIHTPTET ^C DDINE ^C ATPSKVS ^{CG} K	–	1353.92	3	56.2	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CD97	IP100299412	Isoform 2 of CD97 antigen precursor	
87	CNPGFSS ^{FE} IIHTPTET ^C DDINE ^C ATPSKVS ^{CG} K	–	1354.00	3	73.5	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CD97	IP100299412	Isoform 2 of CD97 antigen precursor	
88	W ^{AC} L ^V AGGSKYSEFTSTTSGTGH ^N Q ^T R	+++	950.09	3	74.6	Non-raft	+++	0.75	0.00	5.00	1	0	6.67	2	0	13.33	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CD97	IP100299412	Isoform 2 of CD97 antigen precursor	709
89	LPQKQL ^{LM} ^C QSPGGAGGT ^{VL} GEAPDVLS ^{ML} GADK	–	895.40	4	45.4	Raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CDAN1	IP100217439	Isoform 1 of codanin-1	
90	DSSSL ^S ^C TSGILEER	–	418.88	4	44.1	Raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	CDC42EP4	IP100015894	cdc42 effector protein 4	
91	LG ^C CVVEK ^P QPK	++++	713.55	2	66.0	Non-raft	++++	2.75	0.00	18.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	3	0	20.00	3	0	20.00	3.0	0.0	20.00	CDC42SE1	IP100024972	CDC42 small effector 1	10

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																				Gene Symbol	Acc.Number	Description	Site		
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate									2nd Biological Replicate													
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio					
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio								
99	SSSSSSASAAAAAASSASCSR	+++++	1016.79	2	174.6	Non-raft	+++++	1.25	0.00	8.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CKAP4	IP100141318	Isoform 1 of Cytoskeleton-associated protein 4	100	
			1017.10	2	182.1	Raft	+++++	6.25	0.00	41.67	6	0	40.00	6	0	40.00	6.0	0.0	40.00	5	0	33.33	8	0	53.33	6.5	0.0	43.33	CKAP4	IP100141318	Isoform 1 of cytoskeleton-associated protein 4		
100	ARLVLTSGIVFVISGLVLTLPVCWTAHAIR	+	1107.74	3	44.1	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	CLDN6	IP100011084	Claudin-6	137	
101	LCWVPLLLALGVSGSGGGGDSRQR	+	615.15	4	47.2	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CLSTN2	IP100005491	Calsyntenin-2 precursor	7	
102	KFPFPGHVIVESGNIISFVGYNSCCNIYR	+	1137.37	3	46.9	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	CNBD1	IP100167918	cDNA FLJ35802 fis, clone TESTI2005948	367	
103	LGTDKCDNSSMSLQMGYTQGANQSGQVFGLR	–	1118.02	3	94.0	Non-raft	–	0.75	1.25	0.60	2	0	13.33	0	2	0.00	1.0	1.0	1.00	1	2	0.50	0	1	0.00	0.5	1.5	0.33	CNN2	IP100015262	Calponin-2		
			1118.60	3	102.0	Raft	+	0.75	0.50	1.50	2	1	2.00	1	1	1.00	1.5	1.0	1.50	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CNN2	IP100015262	calponin-2		
104	KCEPIIMTVPR	++	643.99	2	66.3	Raft	++	1.75	0.50	3.50	2	2	1.00	2	0	13.33	2.0	1.0	2.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	CORO1C	IP100008453	coronin-1c	396	
105	SCCTVEAVR	+	433.30	2	44.1	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CROT	IP100292763	Peroxisomal carnitine O-octanoyltransferase	458	
106	GLESTTLADKDGIEICYK	–	922.02	2	58.0	Non-raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CSRP1	IP100442073	Cysteine and glycine-rich protein 1		
107	MMCGAPSATQPATAETQHIAQVR	++	1278.82	2	83.5	Non-raft	++	0.50	0.00	3.33	0	0	0.00	2	0	13.33	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CSTB	IP100021828	Cystatin B	3	
108	CIHVSPNTPNGFMTCSDDFR	+	563.97	4	44.5	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CSTF1	IP100011528	cleavage stimulation factor 50 kDa subunit	415	
109	IGSVLAVFEAAASQASQASQSRVASGQV RPARPER	–	1206.21	3	44.6	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	CTDP1	IP100410256	Isoform 1 of RNA polymerase II subunit A C-terminal domain phosphatase		
110	MSASQLEALCPQVINAALALAAKPSK	+	918.87	3	47.3	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CTNNA1	IP100215948	Isoform 1 of catenin alpha-1	461	
111	YQEAAPNVANNTGPHAAACFGAK	+++++	1159.80	2	113.9	Non-raft	+++++	5.00	0.00	33.33	7	0	46.67	4	0	26.67	5.5	0.0	36.67	5	0	33.33	4	0	26.67	4.5	0.0	30.00	CTNND1	IP100182469	Isoform 1AB of Catenin delta-1	618	
			1160.00	2	109.9	Raft	+++++	4.00	0.00	26.67	4	0	26.67	4	0	26.67	4.0	0.0	26.67	4	0	26.67	4	0	26.67	4.0	0.0	26.67	CTNND1	IP100182469	Isoform 1AB of Catenin delta-1		
112	CVYDGSSEIGSDFK	+	775.53	2	58.1	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	CXADR	IP100019146	Isoform 1 of Coxsackievirus and adenovirus receptor precursor	146	
113	DTANHKNAMSSVATDMSCDHLK	–	798.33	3	50.9	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	CXXC6	IP100303112	CXXC-type zinc finger protein 6		
114	CRLECGEGLRPLVDGTVTAAVCLLGASPPAAGRPLR	+	1303.18	3	47.0	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	CXYorf2	IP100303903	Chromosome X and Y open reading frame 2	22/29/40	
115	EEGPPATATAFLGGCGLSAPTGDYGFPADGKPCVAGALTAIVAGEEELR	+	1209.61	4	50.7	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	DCHS1	IP100064262	Protocadherin-16 precursor	3153	
116	LLATLGLGDVCTLSCVLCASSVLVERR	–	730.32	4	51.8	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	DCTN1	IP100555695	Dynactin 1 isoform 1 variant (Fragment)		
117	LFQLQMC EYLKIVNEIK	–	529.10	4	51.4	Raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	DDEF1	IP100376976	Isoform 1 of 130 kDa phosphatidylinositol 4,5-biphosphate-dependent ARF1 GTPase-activating protein		
118	EILSRCCALEPSLHGACNIR	+	729.03	3	46.3	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	DDO	IP100015389	Isoform DDO-1 of D-aspartate oxidase	258/259/269	
119	VRPCVVYGGADIGQIRDLER	+++	587.02	4	70.5	Raft	+++	1.00	0.00	6.67	2	0	13.33	1	0	6.67	1.5	0.0	10.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	DDX3X	IP100215637	ATP-dependent RNA helicase DDX3X	298	
120	QDLGGTCVNEGCIPTK	–	881.18	2	79.4	Raft	–	0.50	0.50	1.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	1	0	6.67	1	1	1.00	1.0	0.5	2.00	DERP12	IP100382990	DERP12		
121	QDLGGTCVNEGCIPTK	–	880.66	2	52.1	Raft	–	0.00	0.75	0.00	0	1	0.00	0	1	0.00	0.0	1.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	DERP12	IP100382990	DERP12		
122	QDLGGTCVNEGCIPTK	++	818.66	2	94.1	Raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	1	0	6.67	1.0	0.0	6.67	DERP12	IP100382990	DERP12	45/50	
123	NTPCSENKLDIQEK	+	810.05	2	44.6	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	DHX36	IP100027415	Isoform 1 of Probable ATP-dependent RNA helicase DHX36	135	
124	AAECNIVVTQPR	+	650.98	2	65.3	Raft	+	1.50	0.75	2.00	1	1	1.00	2	2	1.00	1.5	1.5	1.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	DHX9	IP100844578	ATP-dependent RNA helicase A	438	
125	DKDDDDGGEDDDANCLICGDEYGPETR	+++++	1019.59	3	75.0	Raft	+++++	1.25	0.00	8.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	DHX9	IP100844578	ATP-dependent RNA helicase A	608	
126	DKDDDDGGEDDDANCLICGDEYGPETR	+	1019.92	3	51.3	Raft	+	0.50	0.25	2.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	1	0.00	1	0	6.67	0.5	0.5	1.00	DHX9	IP100844578	ATP-dependent RNA helicase A	612	
127	TGPLAATRGHDCAR	–	476.10	3	46.2	Non-raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	DIO1	IP100451418	Isoform s of Type I iodothyronine deiodinase		
128	VSMEQCCGGEVQGIQIPGR	+	444.93	4	49.7	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	DLGAP4	IP100445781	CDNA FLJ43393 fis, clone OCBBF2007610, highly similar to Rattus norvegicus PSD-95/SAP90-associated protein-4	232	
129	TTQLGPGRFQMTQEVVCCDECPNVK	–	936.47	3	48.1	Non-raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.					

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																		Gene Symbol	Acc.Number	Description	Site			
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate						2nd Biological Replicate															
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate							Avg. EXP	Avg. CON	Avg. Ratio
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
137	SGDAIVEMVPGKPMCVESFSQYPPLGR	-	989.39	3	62.0	Raft	-	1.00	0.75	1.33	1	2	0.50	2	1	2.00	1.5	1.5	1.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	EEF1A2	IP100014424	Elongation factor 1-alpha 2	
138	SSILLDVKPWDDETDMAKLEECVR	++	932.10	3	73.4	Raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	EEF1B2	IP100178440	Elongation factor 1-beta	161
139	AAAPAPEEEMDECEQALAAEPK	-	1150.75	2	61.4	Non-raft	-	0.75	1.50	0.50	0	3	0.00	2	2	1.00	1.0	2.5	0.40	0	1	0.00	1	0	6.67	0.5	0.5	1.00	EEF1G	IP100000875	Elongation factor 1-gamma	
			1151.41	2	100.0	Raft	+	4.00	2.50	1.60	5	4	1.25	3	4	0.75	4.0	4.0	1.00	4	1	4.00	4	1	4.00	4.0	1.0	4.00	EEF1G	IP100000875	Elongation factor 1-gamma	
140	CELLYEGPPDDEAAMGIK	+	976.54	2	46.2	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	EEF2	IP100186290	Elongation factor 2	369
141	SDPVVSYRETVEESNVLCISK	+	814.56	3	45.3	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	EEF2	IP100186290	Elongation factor 2	591
142	LFASIECEGQLFMTPYDFILAVTTDEPKVAK	-	870.69	4	55.9	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	EFHA2	IP100329209	EF-hand domain-containing family member A2	
143	KPSIAAVVSGMDGHPHSRYCATVR	-	605.73	4	46.0	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	EIF2C3	IP100030602	Eukaryotic translation initiation factor 2c 4	
144	SGGSSTPDEEFTDIPGTK	++++	920.15	2	50.8	Raft	++++	1.00	0.00	6.67	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	2	0	13.33	1.0	0.0	6.67	EIF2S3	IP100297982	Eukaryotic translation initiation factor 2 subunit 3	105
145	GMLLFLCSTMTWKLLK	-	476.11	4	45.8	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	EIF4G2	IP100654814	Hypothetical protein Nbla00315	
146	CGGSPGAYGGGEACAGVKSSGSGR	+	550.27	4	46.5	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	EIF6	IP100375391	integrin beta 4 binding protein isoform c	50
147	APGAASLLCAPDANCGPPDGSQPAAGAGASK	+	699.30	4	46.6	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	EN1	IP100016734	Homeobox protein engrailed-1	171
148	LCLLHKPGGSLGTAKLQDCMSR	+	798.58	3	45.3	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	EXOSC8	IP100552920	Exosome complex exonuclease RRP43	233/234/251
149	AVLTCEQDGSPPSEYTWFKDGIVMPTNPK	-	1100.55	3	85.8	Non-raft	-	0.50	1.00	0.50	0	2	0.00	0	2	0.00	0.0	2.0	0.00	2	0	13.33	0	0	0.00	1.0	0.0	6.67	F11R	IP100001754	Junctional adhesion molecule A precursor	
150	GSCARPFPGTVTK	-	441.09	3	44.9	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	FBN3	IP100438355	Fibrillin-3 precursor	
151	AAPAPGAGAAAGGACGSGGGAGAGAGSGGAAGAGGRLPSR	+	1037.30	3	45.1	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FBXO45	IP100174438	PREDICTED: similar to F-box protein 45 isoform 2	17
	MAAPAPGAGAAAGGACGSGGGAGAGAGSGGAAGAGGRLPSR		1081.69	3	44.7	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FBXO45	IP100174438	PREDICTED: similar to F-box protein 45 isoform 2	
152	LDLNPRTSFSLWFTNPKCK	++++	760.70	3	87.5	Non-raft	++++	2.75	0.00	18.33	2	0	13.33	3	0	20.00	2.5	0.0	16.67	4	0	26.67	2	0	13.33	3.0	0.0	20.00	FER1L3	IP100021048	Isoform 1 of Myoferlin	2013
			760.25	3	84.6	Raft	++++	2.00	0.00	13.33	2	0	13.33	3	0	20.00	2.5	0.0	16.67	1	0	6.67	2	0	13.33	1.5	0.0	10.00	FER1L3	IP100021048	Isoform 1 of Myoferlin	
153	SSLRAGGGGGGGGGGGGGGGGAPVCGASGLCK	+	812.27	3	53.3	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	FEZF2	IP100154618	FEZ family zinc finger 2	121/127
154	CLCVAQFLHPLSQR	+	464.12	4	46.5	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FLJ31033	IP100853133	hypothetical protein LOC91351	300
155	VLPCCQAGLELLDSSDLPASASQSAHGIPR	+	1024.29	3	44.1	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FLJ31222	IP100788134	FLJ31222 protein	22/23
156	TGRSVSACCAPRPTHSSATQASMMLPAPTACSRPVCCLR	+	1064.89	4	71.3	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	FLJ31568	IP100043300	CDNA FLJ31568 fis, clone NT2R12001595	97/98/125
157	TTSPQQEILLQSLEPCGPR	-	539.38	4	46.8	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLJ31713	IP100043522	cDNA FLJ31713 fis, clone NT2R12006487	
158	ALGALVDSCAPGLCPDWSWDASKPVTNAR	+	1081.76	3	47.5	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNA	IP100302592	filamin 1	205
159	ATCAPQHAGAPGPGPADASKVVAK	+	711.22	3	73.7	Non-raft	+	1.50	0.50	3.00	2	2	1.00	0	0	0.00	1.0	1.0	1.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	FLNA	IP100302592	filamin 1	2535
			711.06	3	75.2	Raft	-	1.00	1.00	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNA	IP100302592	filamin 1	
160	CSGPGLSPGMVR	++	580.56	2	61.4	Non-raft	++	1.00	0.00	6.67	2	0	13.33	1	0	6.67	1.5	0.0	10.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FLNA	IP100302592	filamin 1	1165
			581.04	2	82.2	Raft	+	0.75	0.50	1.50	1	1	1.00	2	1	2.00	1.5	1.0	1.50	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNA	IP100302592	filamin 1	
161	CSYQPTMEGVHTVHVTFAGVPIPR	+	876.57	3	65.1	Non-raft	+	1.25	0.75	1.67	2	1	2.00	2	2	1.00	2.0	1.5	1.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FLNA	IP100302592	filamin 1	444
			876.59	3	82.9	Raft	+	1.00	0.50	2.00	2	1	2.00	2	1	2.00	2.0	1.0	2.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNA	IP100302592	filamin 1	
162	IVGPGSAAVPCCK	-	798.37	3	98.6	Non-raft	-	2.50	2.50	1.00	2	4	0.50	4	2	2.00	3.0	3.0	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	FLNA	IP100302592	filamin 1	
	IVGPGSAAVPCCKVEPGLGADNSVVR		798.54	3	99.9	Raft	-	3.00	2.75	1.09	6	4	1.50	4	3	1.33	5.0	3.5	1.43	1	2	0.50	1	2	0.50	1.0	2.0	0.50	FLNA	IP100302592	filamin 1	
163	SPYTVTVGQACNPASCR	-	940.04	2	86.4	Non-raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0									

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																		Gene Symbol	Acc.Number	Description	Site			
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate						2nd Biological Replicate															
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate							Avg. EXP	Avg. CON	Avg. Ratio
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
		–	1155.23	3	109.8	Raft	+	1.00	0.50	2.00	2	1	2.00	2	1	2.00	2.0	1.0	2.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
173	APSVATVGSICDLNLKIPENSSDMSAHVTS PSGR	–	1185.74	3	99.2	Raft	–	0.25	0.25	1.00	1	0	6.67	0	1	0.00	0.5	0.5	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
174	CLATGPGIASTVK	+++	609.43	2	60.3	Non-raft	++++	1.25	0.00	8.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FLNB	IPI00289334	Isoform 1 of Filamin-B	1617
			610.12	2	79.3	Raft	+	1.00	0.50	2.00	2	2	1.00	2	0	13.33	2.0	1.0	2.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
175	DAGYGGISLAVEGPSKVDIQTEDLEDGTC	++	1023.76	3	58.9	Raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	2057
176	GAGIGGLGITVEGPSKINCR	–	706.54	3	49.2	Raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
177	GAGTGGLGLTVEGPCAEK	++	809.68	2	89.6	Raft	++	1.00	0.25	4.00	2	0	13.33	2	1	2.00	2.0	0.5	4.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	1081
178	GLHVVEVTYDDVIPNPPFKVAVTEQCQPS R	+	1119.17	3	43.4	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	1326
179	IEYNDQNDGSCDVK	+	800.46	2	52.4	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	604
180	SGCIVNNLAETVDPK	–	854.65	2	71.8	Non-raft	–	0.25	0.50	0.50	0	2	0.00	1	0	6.67	0.5	1.0	0.50	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
			854.14	2	131.1	Raft	–	1.00	1.00	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
181	SPFVVQVGEACNPNA ^R CR	+++	959.77	2	64.6	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	450
			959.11	2	106.3	Raft	+++	1.00	0.00	6.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
182	SPFVVQVGEACNPNA ^R CR	+++	958.65	2	62.9	Non-raft	+++	0.75	0.00	5.00	1	0	6.67	1	0	6.67	1.0	0.0	6.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FLNB	IPI00289334	Isoform 1 of Filamin-B	455
			959.17	2	130.1	Raft	+++	1.00	0.00	6.67	3	0	20.00	1	0	6.67	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
183	SSFVLVDSKAGSNMLLIGVHGPTTPCEEVS MK	++++	1155.31	3	103.0	Raft	++++	1.25	0.00	8.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	2556
184	SSSETCYSAIPK	–	643.98	2	57.7	Non-raft	+	0.75	0.50	1.50	1	0	6.67	0	1	0.00	0.5	0.5	1.00	1	0	6.67	1	1	1.00	1.0	0.5	2.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
			644.19	2	60.1	Raft	–	0.75	0.75	1.00	1	1	1.00	1	2	0.50	1.0	1.5	0.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	FLNB	IPI00289334	Isoform 1 of Filamin-B	
185	VAVTEGCQPSR	++	573.84	2	53.0	Raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	1326
186	VHSPSGAVEPECHVSELEPKYAVR	–	880.63	3	60.2	Non-raft	+	1.75	1.00	1.75	2	0	13.33	3	2	1.50	2.5	1.0	2.50	0	1	0.00	2	1	2.00	1.0	1.0	1.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
			660.68	4	64.4	Raft	–	0.75	1.25	0.60	0	3	0.00	3	2	1.50	1.5	2.5	0.60	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
187	VVPCCLVTPVTGR	+++	936.57	2	49.7	Non-raft	–	0.25	0.25	1.00	1	0	6.67	0	1	0.00	0.5	0.5	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	991
			620.58	2	52.7	Raft	+++	1.25	0.00	8.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLNB	IPI00289334	Isoform 1 of Filamin-B	
188	MFFT ^{CG} PN ^{EA} MVVSG ^{FC} R	+	1061.71	2	60.3	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLOT1	IPI00027438	Flotillin-1	5
189	MFFT ^{CG} PN ^{EA} MVVSG ^{FC} R	++++	1061.16	2	111.2	Non-raft	++++	7.25	0.00	48.33	9	0	60.00	8	0	53.33	8.5	0.0	56.67	9	0	60.00	3	0	20.00	6.0	0.0	40.00	FLOT1	IPI00027438	Flotillin-1	17
			1069.18	2	121.7	Raft	++++	25.25	0.25	101.00	29	0	193.33	24	0	160.00	26.5	0.0	176.67	26	1	26.00	22	0	146.67	24.0	0.5	48.00	FLOT1	IPI00027438	Flotillin-1	
190	MFFT ^{CG} PN ^{EA} MVVSG ^{FC} R	++++	998.67	2	64.2	Non-raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FLOT1	IPI00027438	Flotillin-1	5/17
			998.67	2	131.0	Raft	++++	3.25	0.00	21.67	4	0	26.67	3	0	20.00	3.5	0.0	23.33	2	0	13.33	4	0	26.67	3.0	0.0	20.00	FLOT1	IPI00027438	Flotillin-1	
191	SPPVMVAGGRVFLPCIQIQIR	++++	799.90	3	110.6	Non-raft	++++	5.75	0.00	38.33	8	0	53.33	7	0	46.67	7.5	0.0	50.00	5	0	33.33	3	0	20.00	4.0	0.0	26.67	FLOT1	IPI00027438	Flotillin-1	34
			799.37	3	123.2	Raft	++++	10.00	0.00	66.67	10	0	66.67	8	0	53.33	9.0	0.0	60.00	11	0	73.33	11	0	73.33	11.0	0.0	73.33	FLOT1	IPI00027438	Flotillin-1	
192	DVPKQMMQMFLGAISLILVCLPIYCR	+	769.49	4	52.3	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	FMR1NB	IPI00166099	Fragile X mental retardation 1 neighbor	199/204
193	RCMVPGESFMQADVINGSVSYQHGR	–	697.09	4	51.7	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	FREM3	IPI00095592	PREDICTED: similar to FRAS1-related extracellular matrix protein 3 precursor	
194	VGKDELFALEQSCAQVVLQAANER	–	880.63	3	60.2	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FSCN1	IPI00163187	Fascin	
			874.02	3	57.6	Raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	FSCN1	IPI00163187	Fascin	
195	KVPGVTAIELGEETCTFR	–	651.04	3	63.7	Raft	–	0.25	0.50	0.50	0	1	0.00	0	1	0.00	0.0	1.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	FXR2	IPI00016250	Fragile X mental retardation syndrome-related protein 2	

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																				Gene Symbol	Acc.Number	Description	Site				
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate								2nd Biological Replicate																
											1st Tech. Replicate				2nd Tech. Replicate				Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate				2nd Tech. Replicate				Avg. EXP	Avg. CON	Avg. Ratio			
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio	Avg. EXP	Avg. CON	Avg. Ratio			3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio								
206	TLESMMACCLSDEVKESK	+	1086.35	2	50.6	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNA11	IP100305551	Guanine nucleotide-binding protein subunit alpha-11	10
207	TLESMMACCLSDEVKESK	+++++	1024.24	2	107.9	Non-raft	+++++	9.75	0.00	65.00	14	0	93.33	10	0	66.67	12.0	0.0	80.00	8	0	53.33	7	0	46.67	7.5	0.0	50.00	GNA11	IP100305551	Guanine nucleotide-binding protein subunit alpha-11	9/10			
			669.27	3	56.7	Raft	+++++	1.75	0.00	11.67	4	0	26.67	3	0	20.00	3.5	0.0	23.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNA11	IP100305551	Guanine nucleotide-binding protein subunit alpha-11				
208	CLLPAEAGGAR	++	529.45	2	53.6	Non-raft	++	0.50	0.00	3.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	GNA12	IP100328744	Guanine nucleotide-binding protein alpha-12 subunit	11			
209	SVLSVCFPGCLLTSGEAEQQR	+++++	1175.93	2	97.5	Non-raft	+++++	2.25	0.00	15.00	3	0	20.00	1	0	6.67	2.0	0.0	13.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	GNA13	IP100290928	Guanine nucleotide-binding protein alpha-13 subunit	14			
210	SVLSVCFPGCLLTSGEAEQQR	+++++	1113.54	2	114.5	Non-raft	+++++	5.00	0.00	33.33	3	0	20.00	4	0	26.67	3.5	0.0	23.33	6	0	40.00	7	0	46.67	6.5	0.0	43.33	GNA13	IP100290928	Guanine nucleotide-binding protein alpha-13 subunit	14/18			
			1112.71	2	70.2	Raft	+++++	2.50	0.00	16.67	2	0	13.33	3	0	20.00	2.5	0.0	16.67	3	0	20.00	2	0	13.33	2.5	0.0	16.67	GNA13	IP100290928	Guanine nucleotide-binding protein alpha-13 subunit				
211	TLESIMACCLSEEAKEAR	+++	1076.50	2	67.7	Non-raft	+++	0.75	0.00	5.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNAQ	IP100288947	Guanine nucleotide binding protein	9			
212	TLESIMACCLSEEAKEAR	+++++	1076.50	2	99.9	Non-raft	+++++	1.50	0.00	10.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	GNAQ	IP100288947	Guanine nucleotide binding protein	10			
			1076.11	2	82.2	Raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNAQ	IP100288947	Guanine nucleotide binding protein				
213	TLESIMACCLSEEAKEAR	+++++	1013.50	2	106.5	Non-raft	+++++	11.25	0.00	75.00	14	0	93.33	11	0	73.33	12.5	0.0	83.33	11	0	73.33	9	0	60.00	10.0	0.0	66.67	GNAQ	IP100288947	Guanine nucleotide binding protein	9/10			
			1014.28	2	105.0	Raft	+++++	3.75	0.00	25.00	3	0	20.00	3	0	20.00	3.0	0.0	20.00	4	0	26.67	5	0	33.33	4.5	0.0	30.00	GNAQ	IP100288947	Guanine nucleotide binding protein				
214	ELAGHTGYLSCCR	-	768.24	2	44.9	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNB1	IP100026268	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	148			
			768.36	2	55.2	Raft	-	0.50	0.50	1.00	0	1	0.00	2	1	2.00	1.0	1.0	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNB1	IP100026268	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1				
215	ELAGHTGYLSCCR	-	768.20	2	45.2	Raft	-	0.00	0.25	0.00	0	0	0.00	0	2	0.00	0.0	1.0	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNB1	IP100026268	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1				
216	KACGDSLTLQTITAGLDPVGR	-	668.93	3	51.3	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GNB2	IP100003348	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2				
217	EEKECMSMR	-	372.16	3	48.3	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GOLGA2	IP100413895	Golgi autoantigen, golgin subfamily A member 2				
218	ATTVPDGCRLGLK	+++++	688.07	2	46.8	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	GPRC5A	IP100022624	Retinoic acid-induced protein 3	9			
			687.64	2	52.8	Raft	+++++	2.00	0.25	8.00	3	1	3.00	1	0	6.67	2.0	0.5	4.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	GPRC5A	IP100022624	Retinoic acid-induced protein 3				
219	QRNPMDYPVEDAFCKPQLVK	+++++	793.89	3	49.5	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GPRC5A	IP100022624	Retinoic acid-induced protein 3	284			
			793.58	3	83.2	Raft	+++++	2.50	0.00	16.67	3	0	20.00	3	0	20.00	3.0	0.0	20.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	GPRC5A	IP100022624	Retinoic acid-induced protein 3				
220	LDPTCLGMADPASVGNVETVPATK	-	796.19	3	60.5	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	GPRIN1	IP100332155	Isoform 1 of G protein-regulated inducer of neurite outgrowth 1				
221	EAGGLCIAQSVRIQER	-	457.88	4	48.8	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	GRM7	IP100292323	Isoform 5 of Metabotropic glutamate receptor 7 precursor				
222	GMFGLMTVSSCLVSK	-	370.84	4	44.8	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	hCG_1745121	IP100788017	PREDICTED: similar to notch1-induced protein				
223	MSVGSILCDQVIYPDSVEGMRR	-	586.79	4	47.4	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	hCG_2042779	IP100735964	PREDICTED: similar to ATP-binding cassette sub-family D member 1				
224	SSFTPCAHHQERR	+	404.10	4	47.6	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	HECW2	IP100017163	HECT, c2 and WW domain containing E3 ubiquitin protein ligase 2	224			
225	MYGCDLGPDGR	+++++	593.03	2	71.4	Non-raft	+++++	1.25	0.00	8.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	2	0	13.33	1	0	6.67	1.5	0.0	10.00	HLA-B	IP100471955	HLA class I histocompatibility antigen, B-50 alpha chain precursor	125			
																												HLA-C	IP100473131	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	125				
226	GCGVVKFESPEVAER	+	536.23	3	70.5	Raft	+	2.25	1.00	2.25	3	1	3.00	2	2	1.00	2.5	1.5	1.67	2	0	13.33	2	1	2.00	2.0	0.5	4.00	HNRPM	IP100171903	heterogeneous nuclear ribonucleoprotein M isoform a	694			
227	LKNNSPGTAECGGGGGGGGGGSGGSGGGGGGGGDK	+	974.24	3	46.9	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	HOXB3	IP100027259	Homeobox protein Hox-B3	153			
228	AAGGDGGNGPGAGIGAATGTGGSSEPSACSDHIPGCSLKEEEK	+	1319.41	3	47.7	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	HOXD9	IP100292734	Homeobox protein Hox-D9	245/263			
229	LLOQDPSSASQF	+++	648.40	2	60.5	Non-raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	HPCA	IP100219103	Neuron-specific calcium-binding protein hippocalcin	185			
			648.62	2	75.9	Raft	+++	0.75	0.00	5.00	1	0	6.67	2	0	13.33	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	HPCA	IP100219103	Neuron-specific calcium-binding protein hippocalcin				
230	LPLALPPASQCGCSGGGGGGGGGSSAGGSGNSRPPR	-	1023.01	3	45.5	Raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	HSPBP1	IP100100748	Isoform 1 of Hsp70-binding protein 1				
231	GGSVLVCSTSCDQPK	+	854.576	2	66.7	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	ICAM1	IP100008494	Intercellular adhesion molecule 1 precursor	48			
232	GGSVLVCSTSCDQPK	-	854.16	2	44.7	Non-raft	-	1.00	1.25	0.80	0	2	0.00	2	2	1.00	1.0	2.0	0.50	1	1	1.00	1	1	1.00	1	0	6.67	1.0	0.5	2.00	ICAM1	IP100008494	Intercellular adhesion molecule 1 precursor	

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																					Gene Symbol	Acc.Number	Description	Site
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate									2nd Biological Replicate												
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio				
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
233	ECGLAAPR	–	409.20	2	48.8	Raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	IRX6	IP100400792	Iroquois-class homeodomain protein IRX-6	
234	SETVLTCA ¹ TGR	++++	569.49	2	87.7	Non-raft	++++	4.75	0.00	31.67	6	0	40.00	5	0	33.33	5.5	0.0	36.67	4	0	26.67	4	0	26.67	4.0	0.0	26.67	ITGA3	IP100215995	Isoform Alpha-3A of Integrin alpha-3 precursor	904
235	SNGLICGGNGVCK	–	674.55	2	77.9	Non-raft	–	0.50	1.00	0.50	0	0	0.00	0	2	0.00	0.0	1.0	0.00	1	1	1.00	1	1	1.00	1.0	1.0	1.00	ITGB1	IP100217561	Isoform Beta-1C of Integrin beta-1 precursor	
236	SNGLICGGNGVCK	–	673.98	2	59.6	Non-raft	–	0.50	0.50	1.00	2	2	1.00	0	0	0.00	1.0	1.0	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ITGB1	IP100217561	Isoform Beta-1C of Integrin beta-1 precursor	
237	VREAMCPGVSGEDSSLLATQVEGQATNLQR	+++	1087.61	3	82.3	Raft	+++	1.25	0.25	5.00	2	1	2.00	2	0	13.33	2.0	0.5	4.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	JUP	IP100554711	Junction plakoglobin	90
238	MEPWCPSPGGGGGGTR	–	391.10	4	49.7	Raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	KCNK2	IP100786999	PREDICTED: similar to Potassium voltage-gated channel subfamily G member 2	
239	MLQSLAGSSCVR	+++	626.47	2	86.3	Non-raft	+++	1.00	0.00	6.67	3	0	20.00	1	0	6.67	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	KCNK1	IP100010476	Potassium channel subfamily K member 1	10
240	VQVTVKPVQHSGLPLMVEAILSVCV ¹ ARSTK	+	1223.29	3	45.1	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	KIF13A	IP100164861	KINESIN-13A1	1058
241	LPAGPDQDCGSRPAPEGAGAGPEQGHSAGGGGW ¹ CRCHTK	+	1034.32	4	46.3	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	KIF26A	IP100788247	Kinesin-like protein KIF26A	45/70
242	MNYYGNYYGGLGYGYGGFDDLGYGYCG ¹ CGSFR	+	924.54	4	47.2	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	KRTAP19-5	IP100373952	Keratin-associated protein 19-5	27
243	GGHSCRGGVDTAAPAGGAPPAHAPGPR	+	638.35	4	50.0	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	LAGE3	IP100032314	L antigen family member 3	33
244	ACGLVASNLNLKPGBC ¹ LR	–	1013.25	2	104.9	Non-raft	–	5.50	6.00	0.92	8	7	1.14	5	6	0.83	6.5	6.5	1.00	4	7	0.57	5	4	1.25	4.5	5.5	0.82	LGALS1	IP100219219	Galectin-1	
			1013.60	2	111.8	Raft	+	21.25	12.75	1.67	26	14	1.86	24	13	1.85	25.0	13.5	1.85	19	14	1.36	16	10	1.60	17.5	12.0	1.46	LGALS1	IP100219219	Galectin-1	
245	ACGLVASNLNLKPGBC ¹ LR	–	1013.74	2	94.8	Non-raft	–	3.00	2.25	1.33	1	3	0.33	2	2	1.00	1.5	2.5	0.60	5	2	2.50	4	2	2.00	4.5	2.0	2.25	LGALS1	IP100219219	Galectin-1	
			676.12	3	65.9	Raft	–	1.25	1.50	0.83	0	1	0.00	1	1	1.00	0.5	1.0	0.50	2	2	1.00	2	2	1.00	2.0	2.0	1.00	LGALS1	IP100219219	Galectin-1	
246	ACGLVASNLNLKPGBC ¹ LR	–	951.23	2	87.4	Non-raft	–	1.25	2.25	0.56	1	2	0.50	2	3	0.67	1.5	2.5	0.60	0	2	0.00	2	2	1.00	1.0	2.0	0.50	LGALS1	IP100219219	Galectin-1	
			951.25	2	108.5	Raft	–	5.50	5.75	0.96	5	7	0.71	7	6	1.17	6.0	6.5	0.92	5	5	1.00	5	5	1.00	5.0	5.0	1.00	LGALS1	IP100219219	Galectin-1	
247	FNAHGDANTIVCNSK	–	883.68	3	71.5	Non-raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LGALS1	IP100219219	Galectin-1	
			796.06	2	97.9	Raft	–	4.00	3.75	1.07	4	4	1.00	4	4	1.00	4.0	4.0	1.00	4	4	1.00	4	3	1.33	4.0	3.5	1.14	LGALS1	IP100219219	Galectin-1	
248	SFVLNLGKDSNNILCHFNPR	++++	763.90	3	90.5	Raft	++++	1.25	0.00	8.33	2	0	13.33	3	0	20.00	2.5	0.0	16.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LGALS1	IP100219219	Galectin-1	43
249	FQAPARETC ¹ VECOQK	–	868.21	2	50.6	Raft	–	0.25	0.25	1.00	1	1	1.00	0	0	0.00	0.5	0.5	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LIMA1	IP100008918	Isoform Beta of LIM domain and actin-binding protein 1	
250	AQNTWGCNSLR	–	654.07	2	45.6	Raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LMNA	IP100021405	Isoform A of Lamin-A/C	
251	SVTVVEDEDEDEDGDDLLHHHHGSH ¹ SSSGDPAEYNLR	+	1358.95	3	57.0	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	LMNA	IP100021405	Isoform A of Lamin-A/C	570
252	TVL ¹ CGTCGQPADKASASGSAQVGGPISSGSSASSVTVTR	–	1256.04	3	155.6	Raft	–	1.75	1.75	1.00	2	2	1.00	0	2	0.00	1.0	2.0	0.50	3	2	1.50	2	1	2.00	2.5	1.5	1.67	LMNA	IP100021405	Isoform A of Lamin-A/C	
253	NNMILCOMDYEEGQLNGTFESQVQ	+	699.13	4	46.6	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	LMO1	IP100396316	Rhombotin-1	138
254	CPGVMGVGSTQSI ¹ LVPGFPKPFSTMNVQWK	–	980.80	4	44.3	Raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	LOC257358	IP100402539	LOC257358 protein	
255	MLL ¹ CTASSSCGCCCGR ¹ LR	+	492.57	4	44.7	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LOC388022	IP100418624	cDNA FLJ29006 fis, clone STM02533	4/11/13/14/15
256	GGSPDSAHGSRPAEAGVSA ¹ QR	+	525.54	4	47.0	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LOC642648	IP100743102	cDNA FLJ41389 fis, clone BRcAN2024563	125
257	EQEMRMGDMG ¹ PCGAINMGDAFSPAPAGNQGPPTMTGMNMNRR	–	1108.87	4	44.9	Raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LOC649009	IP100738041	PREDICTED: similar to paraspeckle protein 1 isoform 1	
258	VLLAGTPEGGGARCMTPPPPSPPR	+	619.58	4	46.2	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LOC651746	IP100235708	PREDICTED: similar to ankyrin repeat domain 33	16
259	MAAAAVQGERSGSGCGSGAGGASNC ¹ GTGSGR	+	957.80	3	53.2	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LOC653566	IP100452747	PREDICTED: similar to Signal peptidase complex subunit 2 (Microsomal signal peptidase 25 kDa subunit) (SPase 25 kDa subunit) isoform 1	17
260	CPEALFQCFLGMESCGIHETTFSIMK	++	1088.00	3	62.2	Raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	LOC653781	IP100479743	protein expressed in prostate, ovary, testis, and placenta 2	965/972
261	CDC ¹ FHMLPTVPGTPGSVSR	++	1146.10	2	72.5	Raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	2	0	13.33	0	0	0.00	1.0	0.0	6.67	LOC730269	IP100787939	PREDICTED: similar to periaxin	2/4
262	RAPPGGGSGTPEPC ¹ CAPR	+	650.88	3	51.6	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00																

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																				Gene Symbol	Acc.Number	Description	Site		
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate									2nd Biological Replicate													
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio					
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio								
268	AVVMISCN R HTLADNFNPVSEER	++++	869.04	3	101.1	Non-raft	++++	1.75	0.00	11.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	2	0	13.33	1	0	6.67	1.5	0.0	10.00	M6PR	IPI00025049	Cation-dependent mannose-6-phosphate receptor precursor	145	
269	GCSLGDVGGHGCGGRR	-	515.84	3	52.1	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MAFK	IPI00065538	cDNA FLJ32205 fs, clone PLACe6003094		
270	LQTCMSGTGMR	-	433.31	3	47.1	Non-raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MAP3K3	IPI00017801	mitogen-activated protein kinase kinase 3 isoform 2		
271	KFDEGENSLGNSFSFTNNVCNQNEIASR	-	1111.64	3	57.7	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MBOAT2	IPI00419221	O-acyltransferase (membrane bound) domain containing 2		
272	GSGSACSL L CCGRDPSEEHSLLVN	+	846.72	3	50.9	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MCOLN1	IPI00003750	Isoform 2 of Mucolipin-1	526/530/531/532	
273	VIVVGNPANTNCLTASK	+	851.13	2	70.5	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MDH1	IPI00291005	Malate dehydrogenase, cytoplasmic	137	
274	SQETECTYFSTPLLLGK	-	959.14	2	44.1	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MDH2	IPI00291006	Malate dehydrogenase, mitochondrial precursor		
275	CPPGRYGP C EQ L CGCLNGGSCDAATGACR	+	1181.91	3	46.4	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MEGF6	IPI00306850	EGF-like-domain, multiple 3	739	
276	LHEYICGGGGGAGGSGHGTGAGR	+	639.24	3	45.8	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	MEGF8	IPI00027310	Isoform 1 of Multiple epidermal growth factor-like domains 8	2325	
277	SAQFEHTLLVTDTCCEILTR	+	745.63	3	62.0	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	METAP1	IPI00022239	Methionine aminopeptidase 1	368	
278	DASSGNLC T EITQGICHMKMK	+	762.58	3	49.3	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	MGC21881	IPI00742024	MGC21881 protein (Fragment)	65	
279	VNMYCVTDDQLICALCK	+	519.21	4	46.2	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	MID1	IPI00029324	Isoform 1 of Midline-1	195/198	
280	CMPAPEIIVEELPASK	+	872.18	2	45.0	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	MKI67	IPI00004233	Isoform Long of Antigen KI-67	3014	
281	MPCESPPEADPTISTR	+	947.12	2	63.3	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MKI67	IPI00004233	Isoform Long of Antigen KI-67	1373	
282	AAAAGGSCPGPGSARGR	-	386.39	4	47.6	Raft	-	0.25	0.25	1.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	1	0.00	0	0	0.00	0.0	0.5	0.00	MLL4	IPI00218823	Isoform 1 of Myeloid/lymphoid or mixed-lineage leukemia protein 4		
283	SDGREVQLEEDPDLQLPFLLPEDGYSCD V VR	+	1179.00	3	48.7	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MLLT4	IPI00023461	Isoform 4 of Afadin	762	
284	RLLYCQR	++	476.58	2	45.6	Non-raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	2	0	13.33	1.0	0.0	6.67	MMP14	IPI00218398	Matrix metalloproteinase-14 precursor	574	
285	LQATTSGRWATELPWMQCWHANSGSALF	+	774.79	4	45.6	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MMP28	IPI00425258	Matrix metalloproteinase-28 precursor	510	
286	SGGGSSVSGGGGGGAGAGCGGPGGALTRR	-	811.98	3	45.9	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MPND	IPI00014455	Mov34/MPN/PAD-1 family protein		
287	VASMAQSAPSEAPSCSPFGK	+++	976.59	2	87.3	Non-raft	+++	1.00	0.00	6.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MPP1	IPI00215610	55 kDa erythrocyte membrane protein	242	
288	DELTNPNSGTLCGSLGK	+	896.46	2	49.4	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MPP2	IPI00217808	Isoform 1 of MAGUK p55 subfamily member 2	338	
289	RDWDNSGPRCGTISSK	++	885.71	2	62.4	Non-raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MPP6	IPI00303280	MAGUK p55 subfamily member 6	298	
290	SSIEVSDTDQEEEEACMAR	+	1123.18	2	95.0	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MPZL3	IPI00375222	QQRG2966	215	
			1122.42	2	72.4	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	MPZL3	IPI00375222	QQRG2966		
291	CCCGLGHMACMVNECEDPSQETITFLYK	+	908.58	4	48.6	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	MSH6	IPI00440122	Sperm protein	237/243	
292	MDPNCSCCTGGSCACAGSCCKCK	+	637.15	4	46.0	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MT1B	IPI00011655	Metallothionein-1B	15/19/21	
293	MDPNCSCAAAGVSCCTCASSCKCK	+	638.26	4	47.5	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	MT1G	IPI00008752	Isoform 1 of Metallothionein-1G	5/14/16/22	
294	DPNYSCTTGGSCCTCAGSCCK	-	475.06	4	47.2	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MT1JP	IPI00329473	MTB		
295	SKIVGAPMHDLLLWNNAVTVTCHSK	+++++	913.74	3	78.9	Non-raft	+++++	1.25	0.00	8.33	2	0	13.33	1	0	6.67	1.5	0.0	10.00	2	0	13.33	0	0	0.00	1.0	0.0	6.67	MTHFD1	IPI00218342	C-1-tetrahydrofolate synthase, cytoplasmic	195	
296	VVTENVPCGTTGTTCCK	+	456.86	4	44.4	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	MUC5AC	IPI00103397	Mucin 5 (Fragment)	953	
297	DQALAEERCLAALTECAASGDGNILAAVDASR	+	798.19	4	51.2	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	MUT	IPI00024934	Methylmalonyl-CoA mutase, mitochondrial precursor	533/540	
298	ALALAALAAVEPACGSR	++	813.55	2	66.6	Raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	1	0	6.67	1.0	0.0	6.67	NDFIP1	IPI00012235	Isoform 1 of NEDD4 family-interacting protein 1	15	
299	FACHSASLTVR	+++++	596.56	2	62.3	Raft	+++++	1.50	0.00	10.00	2	0	13.33	2	0	13.33	2.0	0.0	13.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	NONO	IPI00304596	Non-POU domain-containing octamer-binding protein	145	
300	LPPDPSLPCVLVGPGTGIAFPR	-	555.34	4	47.0	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	NOS3	IPI00218845	Nitric-oxide synthase, endothelial		
301	MED																																

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																		Gene Symbol	Acc.Number	Description	Site			
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate						2nd Biological Replicate															
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate							Avg. EXP	Avg. CON	Avg. Ratio
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
311	AALANLCIGDVTIAIDGENTSNMTHLEAQN R	+	1086.26	3	58.9	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PDLIM1	IP100010414	PDZ and LIM domain protein 1	45
312	RCAGFVVGDLYALLTHSSR	+	517.11	4	47.8	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PEX6	IP100103760	Peroxin Pex6p	627
313	EVLFAFEESIGFLCGTSVLDKDGVSAAVVV AEMASYLETMTNLTK	+	1201.20	4	45.4	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PGM2L1	IP100173346	Phosphoglucutamate-2-like 1	441
314	VSSPGPGPDCCR	–	622.23	2	57.5	Non-raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PGS1	IP100217795	PGS1 protein	
315	AEGSDVANAVLDGADCLIMLSETAKGDYP LEAYR	+	1147.54	3	47.0	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PKM2	IP100220644	pyruvate kinase 3 isoform 2	358
316	NTGIICTIGPASR	–	652.53	2	74.4	Non-raft	–	2.00	2.00	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	PKM2	IP100220644	pyruvate kinase 3 isoform 2	
317	SKPHSEAGTAFIQTQQLHAAMADTFLEHM CR	+	1167.97	3	51.3	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PKM2	IP100220644	pyruvate kinase 3 isoform 2	31
318	NIQTNNKSIGCLFGRS	+++++	877.89	2	83.6	Raft	+++++	2.00	0.00	13.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	3	0	20.00	0	0	0.00	1.5	0.0	10.00	PKP2	IP100005264	Isoform 2 of Plakophilin-2	647
319	DLAGAPPEVGVGCTPQSR	+++	951.13	2	47.1	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PKP3	IP100026952	Plakophilin-3	569
320	AGAQPVGVALQLKPCVCSDSLK	–	566.52	4	44.8	Raft	–	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PLCB1	IP100216920	OTTHUMP00000030235	
321	SGGHRIPGLNCCQGQR	+	537.92	3	53.7	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PLD1	IP100012865	Isoform PLD1A of Phospholipase D1	240/241
322	ADSERLSAPGCWAACTNFSR	+++++	729.58	3	62.3	Non-raft	+++++	2.50	0.00	16.67	5	0	33.33	1	0	6.67	3.0	0.0	20.00	4	0	26.67	0	0	0.00	2.0	0.0	13.33	PLP2	IP100030362	Proteolipid protein 2	12/16
323	VYFAAEDTDCCTR	++	809.69	2	46.0	Non-raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	1	0	6.67	1.0	0.0	6.67	PLSCR1	IP100005181	Phospholipid scramblase 1	148
324	VYFAAEDTDCCTR	+++	810.14	2	83.6	Non-raft	+++	1.00	0.00	6.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PLSCR1	IP100005181	Phospholipid scramblase 1	149
325	VYFAAEDTDCCTR	+++++	747.46	2	105.1	Non-raft	+++++	1.75	0.00	11.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	2	0	13.33	1	0	6.67	1.5	0.0	10.00	PLSCR1	IP100005181	Phospholipid scramblase 1	148/149
			747.96	2	101.6	Raft	+++++	2.00	0.00	13.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	PLSCR1	IP100005181	Phospholipid scramblase 1	
326	SGAGQLPGQAAEESNCCAR	+++++	987.72	2	95.9	Non-raft	+++++	2.25	0.00	15.00	3	0	20.00	2	0	13.33	2.5	0.0	16.67	3	0	20.00	1	0	6.67	2.0	0.0	13.33	PLSCR3	IP100216127	Phospholipid scramblase 3	125
327	SGAGQLPGQAAEESNCCAR	+++++	988.17	2	96.1	Non-raft	+++++	1.50	0.00	10.00	1	0	6.67	2	0	13.33	1.5	0.0	10.00	1	0	6.67	2	0	13.33	1.5	0.0	10.00	PLSCR3	IP100216127	Phospholipid scramblase 3	126
328	SGAGQLPGQAAEESNCCAR	+++++	925.55	2	99.4	Non-raft	+++++	2.25	0.00	15.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	4	0	26.67	2	0	13.33	3.0	0.0	20.00	PLSCR3	IP100216127	Phospholipid scramblase 3	125/126
			925.59	2	105.2	Raft	+++++	2.00	0.00	13.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	PLSCR3	IP100216127	Phospholipid scramblase 3	
329	SGAGQLPGQAAEESNCCARLCCGAR	+	818.19	3	45.6	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PLSCR3	IP100216127	Phospholipid scramblase 3	125/126/1 30/131
			818.17	3	47.0	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	PLSCR3	IP100216127	Phospholipid scramblase 3	
330	VVVGPCWTCGCTDITNFEVK	+++++	1009.18	2	60.0	Non-raft	+++++	1.00	0.00	6.67	2	0	13.33	0	0	0.00	1.0	0.0	6.67	1	0	6.67	1	0	6.67	1.0	0.0	6.67	PLSCR3	IP100216127	Phospholipid scramblase 3	211/214/2 16
331	VRGPCSTYGCSDSDSVFEVK	++++	996.39	2	61.1	Non-raft	++++	1.25	0.00	8.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PLSCR4	IP100016776	Phospholipid scramblase 4	250/255
332	MAEASSANLGSQCEEKR	+	439.73	4	45.3	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PMF1	IP100178359	Isoform 3 of Polyamine-modulated factor 1	13
333	YFVKDVLGCVCVNPNR	–	443.20	4	48.3	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	POLA2	IP100290272	DNA polymerase subunit alpha B	
334	ALEYNSNGIFDCQSPSTPFMGSLR	+	635.36	4	49.0	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	PPFIBP1	IP100179172	Isoform 2 of Liprin-beta-1	35
335	KITIADCQGLE	–	595.74	2	92.3	Non-raft	–	1.75	2.00	0.88	2	2	1.00	2	2	1.00	2.0	2.0	1.00	2	2	1.00	1	2	0.50	1.5	2.0	0.75	PPIAP19	IP100374732	PREDICTED: similar to peptidylprolyl isomerase A isoform 1	
			595.85	2	96.3	Raft	–	2.00	1.75	1.14	2	2	1.00	2	2	1.00	2.0	2.0	1.00	2	2	1.00	2	1	2.00	2.0	1.5	1.33	PPIAP19	IP100374732	PREDICTED: similar to peptidylprolyl isomerase A isoform 1	
336	MLSSSPASCSTSPDPGENPCCK	+	566.68	4	47.8	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PPP1R14D	IP100015106	Protein phosphatase 1 regulatory subunit 14D	47
337	SDGSACNSGISGGRGR	+	371.20	4	47.5	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PRAC	IP100064590	small nuclear protein PRAC	84
338	TREEECHFYAGGQVYPGEASR	+++	796.40	3	57.3	Non-raft	+++	0.75	0.00	5.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PRDX4	IP100011937	Peroxisredoxin-4	51
339	GSDHTDVCGNVVSSGGSSSSGGSDK	+	781.39	3	58.7	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	PROSAP1P1	IP100028588	Protein KIAA0552	112
340	SLICISISNEVPEHPVSPVSNHVVYER	+++++	1021.73																													

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																		Gene Symbol	Acc.Number	Description	Site			
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate						2nd Biological Replicate															
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate							Avg. EXP	Avg. CON	Avg. Ratio
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
350	ALAEQEWGCPFMETSAK	++++	884.82	2	77.8	Non-raft	++++	1.25	0.00	8.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	2	0	13.33	1	0	6.67	1.5	0.0	10.00	RAP2C	IPI00009607	Ras-related protein Rap-2c precursor	140
351	MHLPGCAPAMADGSFSLAGHLR	-	597.43	4	45.8	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	RAX	IPI00021025	Retinal homeobox protein Rx	
352	NLEQSSKAGDMGNVCYSGQQQEGGVSEEMK	+	786.56	4	44.4	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	RFTN1	IPI00749454	Raftlin	494
353	CVLVGDSAVGKTSLLVR	-	430.45	4	45.8	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	RHOH	IPI00018882	Rho-related GTP-binding protein RhoH	
			430.29	4	47.1	Raft	-	0.25	0.25	1.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	1	0.00	0	0	0.00	0.0	0.5	0.00	RHOH	IPI00018882	Rho-related GTP-binding protein RhoH	
354	LLAQEACVAGWALPHNRMQALTSCECTICPD _{CFR}	++	982.66	4	47.8	Non-raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	2	0	13.33	0	0	0.00	1.0	0.0	6.67	RNF31	IPI00094740	Isoform 1 of RING finger protein 31	702/717/719/722/725
			982.60	4	61.3	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	RNF31	IPI00094740	Isoform 1 of RING finger protein 31	
355	LPPQALQLSSPCSSDSL _{CSR}	+	576.74	4	49.3	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	ROBO4	IPI00103871	Isoform 1 of Roundabout homolog 4 precursor	625
356	AKVDEFFLPGHMVSDEYEQLSSEALEAAR	++	1076.16	3	131.6	Raft	++	2.75	0.75	3.67	4	0	26.67	0	3	0.00	2.0	1.5	1.33	3	0	20.00	4	0	26.67	3.5	0.0	23.33	RPL10	IPI00554723	60S ribosomal protein L10	49
357	FSVCVLGDQOHCDEAK	++++	952.76	2	69.0	Raft	++++	1.50	0.00	10.00	3	0	20.00	2	0	13.33	2.5	0.0	16.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	RPL10A	IPI00412579	60S ribosomal protein L10a	74
358	CTGGEVGATSSALAPK	-	681.46	2	77.1	Raft	-	2.00	2.00	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	RPL12	IPI00024933	60S ribosomal protein L12	
359	HPHDIIDDSNGAVECPAS	+++++	995.55	2	74.8	Raft	+++++	3.50	0.00	23.33	3	0	20.00	4	0	26.67	3.5	0.0	23.33	4	0	26.67	3	0	20.00	3.5	0.0	23.33	RPL12	IPI00024933	60S ribosomal protein L12	162
360	VVYLRC _T GGGEVGATSSALAPK	-	665.58	3	45.5	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	RPL12	IPI00024933	60S ribosomal protein L12	
361	GC _T GTVLLSGPR	+	530.65	2	54.2	Raft	+	0.50	0.25	2.00	1	1	1.00	0	0	0.00	0.5	0.5	1.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	RPL18	IPI00215719	60S ribosomal protein L18	134
362	EYRDLTTAGAVTQCYR	++	616.79	3	67.5	Raft	++	0.50	0.00	3.33	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	1	0	6.67	0.5	0.0	3.33	RPL18A	IPI00026202	60S ribosomal protein L18a	109
363	TGVHHYSGNNIELGTACGKYR	+	611.40	4	47.5	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	RPL30	IPI00219156	60S ribosomal protein L30	85
364	VCTLAHDPGDSDIIR	-	851.14	2	79.9	Raft	-	2.00	2.00	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	RPL30	IPI00219156	60S ribosomal protein L30	
365	SACGVC _{CFR} PGR	++	488.74	2	52.6	Raft	++	0.50	0.00	3.33	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	1	0	6.67	0.5	0.0	3.33	RPL34	IPI00219160	60S ribosomal protein L34	46
366	ACARPLISVYSEKGESSGK	-	675.69	3	74.5	Raft	-	2.00	1.50	1.33	4	2	2.00	2	1	2.00	3.0	1.5	2.00	2	2	1.00	0	1	0.00	1.0	1.5	0.67	RPL4	IPI00003918	60S ribosomal protein L4	
367	SGQGAGFNMC _{CFR} R	+	564.13	2	56.2	Raft	+	1.50	0.50	3.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	2	1	2.00	1	1	1.00	1.5	1.0	1.50	RPL4	IPI00003918	60S ribosomal protein L4	96
368	AQLNIGNVLPVGTMP _{CFR} EGTIVC _{CFR} LEEKPGDR GK	++	867.04	4	46.5	Raft	++	0.50	0.00	3.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	1	0	6.67	0	0	0.00	0.5	0.0	3.33	RPL8	IPI00012772	60S ribosomal protein L8	114
369	AQLNIGNVLPVGTMP _{CFR} EGTIVC _{CFR} LEEKPGDR GK	+	1155.52	3	62.9	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	RPL8	IPI00012772	60S ribosomal protein L8	115
370	AGAIAPCEVTVPAQNTGLGPEK	+++++	1140.48	3	48.1	Non-raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	RPLP0	IPI00008530	60S acidic ribosomal protein P0	119
			1062.85	2	90.5	Raft	+++++	4.50	0.50	9.00	6	1	6.00	5	1	5.00	5.5	1.0	5.50	4	0	26.67	3	0	20.00	3.5	0.0	23.33	RPLP0	IPI00008530	60S acidic ribosomal protein P0	
371	ALANVNI _{CFR} SL _{CFR} CVN _{CFR} GAGGPAPAA _{CFR} GAAPAG GPAPSTAAAPAEK	+++++	939.43	4	81.9	Raft	+++++	1.25	0.00	8.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	2	0	13.33	1	0	6.67	1.5	0.0	10.00	RPLP1	IPI00008527	60S acidic ribosomal protein P1	61
372	KLLMMAGIDD _{CFR} CYTSAR	+++++	894.63	2	86.6	Raft	+++++	2.00	0.00	13.33	4	0	26.67	1	0	6.67	2.5	0.0	16.67	1	0	6.67	2	0	13.33	1.5	0.0	10.00	RPS2	IPI00013485	40S ribosomal protein S2	222
373	CCLTY _{CFR} CNKPEDK	-	907.57	2	48.6	Raft	-	0.25	1.00	0.25	0	2	0.00	0	2	0.00	0.0	2.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	RPS27A	IPI00179330	ubiquitin and ribosomal protein S27a precursor	
374	ECP _{CFR} SD _{CFR} CAGGVFMASHFDR	+	1092.74	2	47.7	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	RPS27A	IPI00179330	ubiquitin and ribosomal protein S27a precursor	126
375	TGSQGC _{CFR} QTVRVEFMDDTSR	-	749.24	3	49.7	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	RPS28	IPI00719622	40S ribosomal protein S28	
			749.53	3	86.5	Raft	-	3.00	2.50	1.20	3	6	0.50	2	1	2.00	2.5	3.5	0.71	4	2	2.00	3	1	3.00	3.5	1.5	2.33	RPS28	IPI00719622	40S ribosomal protein S28	
376	MKLNISFPATG _{CFR} CQK	+	769.64	2	91.0	Raft	+	2.25	1.50	1.50	2	2	1.00	3	2	1.50	2.5	2.0	1.25	2	2	1.00	2	0	13.33	2.0	1.0	2.00	RPS6	IPI00021840	40S ribosomal protein S6	12
377	YVDIAIP _{CFR} CNNK	+	625.55	2	46.9	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	RPSA	IPI00553164	40S ribosomal protein SA	163
378	LLVVTDP _{CFR} PRADHQPLTEASYVNLPTIAL _{CFR} NT _{CFR} DSLPR	+	1279.00	3	113.9	Raft	+	2.25	1.00	2.25	4	1	4.00	2	2	1.00	3.0	1.5	2.00	1	0	6.67	2	1	2.00	1.5	0.5	3.00	RPSA	IPI00553164	40S ribosomal protein SA	148
379	FCHQLDFSTSGAL _{CFR} CVALNK	+	545.94	4	56.3	Non-raft																										

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																		Gene Symbol	Acc.Number	Description	Site			
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate						2nd Biological Replicate															
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate									
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
391	GLAAAEPTANGGLALASIEDQGAAGGYGSRDQVR	+++++	1140.28	3	176.5	Non-raft	+++++	5.25	0.00	35.00	6	0	40.00	7	0	46.67	6.5	0.0	43.33	4	0	26.67	4	0	26.67	4.0	0.0	26.67	SLC1A5	IP100019472	Neutral amino acid transporter B(0)	39
392	SSGPGMAPSA <u>CC</u> SCPAALQR	+++++	947.55	2	77.9	Non-raft	+++++	2.75	0.00	18.33	3	0	20.00	2	0	13.33	2.5	0.0	16.67	3	0	20.00	3	0	20.00	3.0	0.0	20.00	SLC26A11	IP100410334	Sulfate/anion exchanger	23/24/25
393	A <u>C</u> VFGNEPKASDEVPLAPR	+++	1001.13	2	86.8	Non-raft	+++	1.00	0.00	6.67	3	0	20.00	1	0	6.67	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SLC35B2	IP100384867	Isoform 2 of Adenosine 3'-phospho 5'-phosphosulfate transporter 1	80
394	GL <u>C</u> FPLVK	++	438.60	2	49.2	Non-raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SLC35B2	IP100384867	Isoform 2 of Adenosine 3'-phospho 5'-phosphosulfate transporter 1	73
395	SLNPATIPVPLPKLLSLPL <u>S</u> QK	+++++	870.73	3	84.6	Non-raft	+++++	1.50	0.00	10.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	SLC5A6	IP100031822	Sodium-dependent multivitamin transporter	577
396	G <u>C</u> KVLLNIGQQMLR	+++++	808.44	2	91.6	Non-raft	+++++	2.25	0.00	15.00	4	0	26.67	2	0	13.33	3.0	0.0	20.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	SLC7A1	IP100027728	High-affinity cationic amino acid transporter 1	3
397	TLTELNK <u>CC</u> GL <u>C</u> VCPNR	+++++	985.76	2	92.2	Non-raft	+++++	1.50	0.00	10.00	2	0	13.33	0	0	0.00	1.0	0.0	6.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	SNAP23	IP100010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	79/80/83/85/87
			985.76	2	105.4	Raft	+++++	3.00	0.00	20.00	3	0	20.00	2	0	13.33	2.5	0.0	16.67	3	0	20.00	4	0	26.67	3.5	0.0	23.33	SNAP23	IP100010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	
398	TTWGDGGGENSP <u>C</u> NVVS	+++++	876.12	2	89.2	Non-raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SNAP23	IP100010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	112
			876.74	2	91.4	Raft	+++++	3.75	0.00	25.00	4	0	26.67	5	0	33.33	4.5	0.0	30.00	3	0	20.00	3	0	20.00	3.0	0.0	20.00	SNAP23	IP100010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	
399	ANNPEQNRLSE <u>C</u> EEQAK	+	980.66	2	68.0	Raft	+	1.25	0.75	1.67	2	2	1.00	1	1	1.00	1.5	1.5	1.00	2	0	13.33	0	0	0.00	1.0	0.0	6.67	SND1	IP100140420	Staphylococcal nuclease domain-containing protein 1	152
400	VQFQDMCATIGVDPPLASGK	+	666.89	3	45.7	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SNF8	IP100101524	Isoform 1 of Vacuolar sorting protein SNF8	72
401	SIGVPIKVLHEAEGHIVT <u>C</u> ETNTGEVYR	++++	1032.25	3	61.4	Raft	++++	1.75	0.25	7.00	1	0	6.67	1	1	1.00	1.0	0.5	2.00	3	0	20.00	2	0	13.33	2.5	0.0	16.67	SNRPD3	IP100017964	Small nuclear ribonucleoprotein Sm D3	10
402	NGGGGGGGGSLH <u>C</u> AGNGGGGGGGPR	+	496.18	4	44.5	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SNX27	IP100640980	sorting nexin family member 27	30
403	STCPSAAPSASAPAMTTVENK	+	1011.01	2	46.7	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SPECC1L	IP100178072	cytospin-A	79
404	<u>C</u> GCAGCGRHEEAR	-	492.81	3	47.1	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	SPRED3	IP100397716	Sprouty-related, EVH1 domain-containing protein 3	
405	NMVHPNVICDGCNGPVVGTR	+	1104.10	2	55.7	Non-raft	++	0.75	0.00	5.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SQSTM1	IP100179473	48 kDa protein	127
			1104.78	2	83.8	Raft	-	0.75	0.75	1.00	1	1	1.00	0	1	0.00	0.5	1.0	0.50	2	0	13.33	0	1	0.00	1.0	0.5	2.00	SQSTM1	IP100179473	48 kDa protein	
406	NMVHPNVICDGCNGPVVGTR	+	736.51	3	58.7	Non-raft	+	0.50	0.25	2.00	1	0	6.67	1	1	1.00	1.0	0.5	2.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SQSTM1	IP100179473	48 kDa protein	131
			737.27	3	86.2	Raft	++	1.75	0.50	3.50	2	1	2.00	2	1	2.00	2.0	1.0	2.00	1	0	6.67	2	0	13.33	1.5	0.0	10.00	SQSTM1	IP100179473	48 kDa protein	
407	SSSQSS <u>CC</u> SDSPKPGGNVEGATQSLAEQM R	-	1084.37	3	57.9	Non-raft	+	0.50	0.25	2.00	2	0	13.33	0	1	0.00	1.0	0.5	2.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SQSTM1	IP100179473	48 kDa protein	
			1085.08	3	94.3	Raft	-	1.75	1.50	1.17	1	2	0.50	2	1	2.00	1.5	1.5	1.00	2	2	1.00	2	1	2.00	2.0	1.5	1.33	SQSTM1	IP100179473	48 kDa protein	
408	SSSQSS <u>CC</u> SDSPKPGGNVEGATQSLAEQM R	-	1084.41	3	49.2	Non-raft	-	0.00	0.75	0.00	0	2	0.00	0	1	0.00	0.0	1.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	SQSTM1	IP100179473	48 kDa protein	
			1084.77	3	79.2	Raft	-	0.25	0.25	1.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	1	0.00	0.0	0.5	0.00	SQSTM1	IP100179473	48 kDa protein	
409	FPNGTASSPSSPSPPG <u>S</u> CEGGGSRGPGA GAADGMEEPGR	+	1269.19	3	47.4	Non-raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	SSTR1	IP100027804	Somatostatin receptor type 1	21
410	ALDLDS <u>CK</u> EAADGYQR	-	921.76	2	55.1	Non-raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	STIP1	IP100013894	Stress-induced-phosphoprotein 1	
411	WL <u>C</u> VGECEGGALGRR	+	535.96	3	47.7	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	STK11IP	IP100885068	Isoform 2 of serine/threonine kinase 11-interacting protein	734/738
412	LQDGCNNLLTHT <u>C</u> TRG <u>CS</u> S	-	566.52	4	46.9	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	STK32B	IP100293334	Isoform 1 of Serine/threonine-protein kinase 32B	
413	GPGLFFILP <u>C</u> TDSFIK	+++++	878.20	2	62.2	Non-raft	+++	0.75	0.00	5.00	1	0	6.67	2	0	13.33	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	STOM	IP100219682	Erythrocyte band 7 integral membrane protein	87
			878.07	2	79.7	Raft	+++++	2.75	0.00	18.33	4	0	26.67	3	0	20.00	3.5	0.0	23.33	2	0	13.33	2	0	13.33	2.0	0.0	13.33	STOM	IP100219682	Erythrocyte band 7 integral membrane protein	
414	GGNDT <u>C</u> FLEGLLGPLLSPPLGSPPL <u>C</u> LTP GPFLLGMLSQLP	+	1130.25	4	54.5	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	STRC	IP100170605	Stereocilin precursor	568/590
415	KPPGSGRWLGLAAGTATLPSSLCPGVQASR	+	980.10	3	46.7	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TACC2	IP100743514	Similar to Transforming acidic coiled-coil-containing protein 2	82
416	WASGLTPAQN <u>C</u> PR	+	701.75	2	45.5	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TAPBP	IP100007327	Isoform 1 of Tapasin precursor	115
417	LDGHT <u>S</u> CLTWTPFNK	+	574.34	3	46.3	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1												

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																				Gene Symbol	Acc.Number	Description	Site	
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate									2nd Biological Replicate												
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON					Avg. Ratio
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
426	EAALPILEPVLGQEQAAPD Q CVLFADAP EPGQALPVEEEAVTLAR	++	1223.72	4	48.8	Raft	++	0.50	0.00	3.33	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TNKS1BP1	IPI00304589	182 kDa tankyrase 1-binding protein	631
427	CTKEEHL CT QR	+++	737.16	2	62.7	Non-raft	++++	1.25	0.00	8.33	2	0	13.33	1	0	6.67	1.5	0.0	10.00	1	0	6.67	1	0	6.67	1.0	0.0	6.67	TPM3	IPI00178083	29 kDa protein	209
			737.07	2	75.3	Raft	-	0.75	0.75	1.00	1	2	0.50	2	1	2.00	1.5	1.5	1.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TPM3	IPI00178083	29 kDa protein	
428	ESQSLGGQ S CAGEPDEELVGAFPIFVR	+	735.16	4	45.9	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	TRAIP	IPI00306611	TRAF-interacting protein	373
429	NQSLPVMVGSFAAP V CTSSPKMGVLK	+	898.97	3	45.2	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	TRAK2	IPI00297257	Trafficking kinesin-binding protein 2	902
430	MQSLSEAPNSDSLAPKPPSNSAS D CTASTTE LK	-	1119.37	3	43.5	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	TSHZ2	IPI00032988	Teashirt homolog 2	
431	G S CLGSVLLSPTSTAPATSSSTVTTAK	+	632.46	4	53.8	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TSHZ3	IPI00001743	Teashirt homolog 3	801
432	VADEALKVDD CD CHPEFSPSSQPPK	+	734.98	4	47.9	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TTC3	IPI00023977	Isoform TRPDI of Tetraatricopeptide repeat protein 3	422
433	M I CCQLYSIKPFHIDGFK	-	515.37	4	45.6	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	TTLL6	IPI00297940	cDNA FLJ40073 fis, clone TESTI2000272.	
434	AYHEQLSVAEITNA CF EPAQNQMVK	+	898.88	3	59.4	Non-raft	-	0.25	0.25	1.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	1	0	6.67	0.5	0.0	3.33	TUBA4A	IPI00007750	Tubulin alpha-1 chain	295
			898.89	3	57.4	Raft	+++	0.75	0.00	5.00	1	0	6.67	1	0	6.67	1.0	0.0	6.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	TUBA4A	IPI00007750	Tubulin alpha-1 chain	
435	SIQFVDW CT PTGFK	-	1112.74	3	62.9	Non-raft	+	0.50	0.25	2.00	2	1	2.00	0	0	0.00	1.0	0.5	2.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TUBA4A	IPI00007750	Tubulin alpha-1 chain	
			765.08	2	47.5	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TUBA4A	IPI00007750	Tubulin alpha-1 chain	
436	MREIVHIQAG QC GNQIGAK	+	690.78	3	97.0	Non-raft	+	3.50	1.75	2.00	4	3	1.33	6	4	1.50	5.0	3.5	1.43	3	0	20.00	1	0	6.67	2.0	0.0	13.33	TUBB2C	IPI00007752	Tubulin beta-2C chain	12
			685.61	3	80.5	Raft	-	0.25	0.75	0.33	0	2	0.00	1	1	1.00	0.5	1.5	0.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	TUBB2C	IPI00007752	Tubulin beta-2c chain	
437	NMMA AC DP R	+	505.02	2	52.2	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	TUBB2C	IPI00007752	Tubulin beta-2c chain	303
438	VTEAP C YPGAPSTEASQGTGPQEPTSARA	+	954.57	3	64.0	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	TXLNA	IPI00470779	Alpha-taxilin	523
439	LR C GGTAEEILDV	+++	688.50	2	55.8	Non-raft	+++	0.75	0.00	5.00	1	0	6.67	1	0	6.67	1.0	0.0	6.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	UGCG	IPI00003861	Ceramide glucosyltransferase	384
440	AASNAAAAAAGLDFAPGL C APR	-	719.13	3	49.9	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	UNCX	IPI00248578	PREDICTED: similar to Unc4.1 homeobox	
441	TAGQPEGGPGADFGQ S CPAEAGRDTLSR	-	960.79	3	103.0	Raft	-	1.50	1.50	1.00	2	2	1.00	2	2	1.00	2.0	2.0	1.00	1	1	1.00	1	1	1.00	1.0	1.0	1.00	USP10	IPI00291946	Ubiquitin carboxyl-terminal hydrolase 10	
442	TPSYSISSTLNQPAPEH L CTASK	-	871.77	3	58.1	Raft	-	0.00	0.25	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	USP10	IPI00291946	Ubiquitin carboxyl-terminal hydrolase 10	
443	ELADNS CL RPIDRNGK	+	601.73	3	51.8	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	USP40	IPI00398007	ubiquitin specific protease 40	810
444	RACSDVT T VAK	-	384.46	3	48.8	Raft	-	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	UTS2D	IPI00792987	9 kDa protein	
445	CV FEMPENENDKLNMEPSK	+++	1120.68	2	51.4	Non-raft	+++	0.75	0.00	5.00	2	0	13.33	1	0	6.67	1.5	0.0	10.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	VAPA	IPI00170692	vesicle-associated membrane protein-associated protein A isoform 2	128
446	VC EDLDTSVNLAWTSGT N CTR	+	1205.97	2	61.1	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	VDAC2	IPI00024145	Isoform 1 of Voltage-dependent anion-selective channel protein 2	225
447	VC EDLDTSVNLAWTSGT N CTR	+	1206.48	2	60.3	Non-raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	VDAC2	IPI00024145	Isoform 1 of Voltage-dependent anion-selective channel protein 2	242
448	QVQSL TC VDALKGTNESLER	-	1161.32	2	125.5	Raft	-	2.25	2.50	0.90	2	4	0.50	3	2	1.50	2.5	3.0	0.83	2	3	0.67	2	1	2.00	2.0	2.0	1.00	VIM	IPI00418471	Vimentin	
449	GQEDAVAP GC KASGR	+	483.15	3	46.9	Raft	+	0.25	0.00	1.67	1	0	6.67	0	0	0.00	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	VSIG8	IPI00479090	Novel protein	29
450	ASPPSS SC NISSGEMQK	+	428.14	4	44.6	Raft	+	0.25	0.00	1.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	1	0	6.67	0	0	0.00	0.5	0.0	3.33	VWF	IPI00023014	von Willebrand factor precursor	210
451	TW CP PC L PAPSPAQMIPSPAVTGSQRPPW GSQR	+	936.29	4	58.0	Raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	WDR90	IPI00640784	cDNA FLJ44660 fis, clone BRACe3002344, weakly similar to Vegetatible incompatibility protein HET-E-1	983
452	CHGVSG S CTV RT CWR	-	445.30	4	46.2	Non-raft	-	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	WNT9A	IPI00220170	Protein Wnt-9a precursor	
453	ASGGRC GC PGAGAAAGSGGGGDAPGPAGR	+	550.35	4	49.5																											

No.	Sequences	Prob. Both	Precursor m/z	Charge	Score	Fraction	Prob. Each	Spectral Counts																		Gene Symbol	Acc.Number	Description	Site			
								Avg. EXP	Avg. CON	Avg. Ratio	1st Biological Replicate						2nd Biological Replicate															
											1st Tech. Replicate			2nd Tech. Replicate			Avg. EXP	Avg. CON	Avg. Ratio	1st Tech. Replicate			2nd Tech. Replicate							Avg. EXP	Avg. CON	Avg. Ratio
											1st EXP	1st CON	1st Ratio	2nd EXP	2nd CON	2nd Ratio				3rd EXP	3rd CON	3rd Ratio	4th EXP	4th CON	4th Ratio							
466	GGVNPFTNGCCNNVSR	+++++	820.05	2	82.9	Non-raft	+++++	4.50	0.00	30.00	5	0	33.33	4	0	26.67	4.5	0.0	30.00	4	0	26.67	5	0	33.33	4.5	0.0	30.00	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	236/237
			820.10	2	97.5	Raft	+++++	6.00	0.00	40.00	6	0	40.00	6	0	40.00	6.0	0.0	40.00	6	0	40.00	6	0	40.00	6.0	0.0	40.00	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	
467	VLCSSPAPR	+++++	465.19	2	56.9	Non-raft	++	0.50	0.00	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	2	0	13.33	0	0	0.00	1.0	0.0	6.67	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	245
			465.24	2	66.3	Raft	+++++	5.00	0.00	33.33	6	0	40.00	5	0	33.33	5.5	0.0	36.67	4	0	26.67	5	0	33.33	4.5	0.0	30.00	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	
468	TFTSPCTEEPR	+	708.49	2	45.0	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ZDHHC6	IPI00008350	Isoform 1 of Probable palmitoyltransferase ZDHHC6	343
469	YKVIEDYSGACCLNK	+++	902.30	2	103.4	Non-raft	+++	1.00	0.00	6.67	2	0	13.33	2	0	13.33	2.0	0.0	13.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ZDHHC6	IPI00008350	Isoform 1 of Probable palmitoyltransferase ZDHHC6	328/329
470	GCCGNVEHVLCSPLAPR	++	878.57	2	75.6	Non-raft	++	0.50	0.00	3.33	2	0	13.33	0	0	0.00	1.0	0.0	6.67	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ZDHHC8	IPI00385426	Isoform 1 of Probable palmitoyltransferase ZDHHC8	236/237/245
471	SKYCLK	–	371.05	2	46.9	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	1	0.00	0	0	0.00	0.0	0.5	0.00	ZFP161	IPI00307325	Zinc finger protein 161 homolog	
472	MIPICPVVSFTYVPSRLGEDAK	+++	1232.93	2	58.6	Raft	+++	1.00	0.00	6.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	2	0	13.33	1	0	6.67	1.5	0.0	10.00	ZFR	IPI00333858	117 kDa protein	5
473	TFCSLSCLSSYEK	–	533.45	3	44.2	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	ZMYM1	IPI00470588	Novel protein	
			533.45	3	44.1	Raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ZMYM1	IPI00470588	Novel protein	
474	STGGGGDGGGGGGAEGTGAGGCCCGGLR	+	890.57	3	45.0	Non-raft	+	0.25	0.00	1.67	0	0	0.00	1	0	6.67	0.5	0.0	3.33	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ZNF282	IPI00003798	Zinc finger protein 282	496/499/500
475	DALEMICNLESEGDEK	–	899.17	2	51.9	Raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ZNF292	IPI00164352	PREDICTED: similar to Zinc finger protein 292 isoform 1	
476	ACEIKDNSQCQGGPFTQTQDSIVNEK	–	946.86	3	44.2	Non-raft	–	0.00	0.25	0.00	0	0	0.00	0	1	0.00	0.0	0.5	0.00	0	0	0.00	0	0	0.00	0.0	0.0	0.00	ZNF441	IPI00175390	Zinc finger protein 441	

Category	Criterion	Avg. Ratio	1st Biological Replicate		2nd Biological Replicate	
			Total EXP	Avg. Ratio	Total EXP	Avg. Ratio
Highly probable	+++++	≥3.3	≥2	≥3.0	≥2	≥3.0
Probable	+++++	≥7.0	Not satisfy the +++++ criterion			
	+++	≥5.0 and <7.0				
	++	≥3.3 and <5.0				
Others	+	≥1.5 and <3.3				
	–	<1.5				

- Note 1.** No. = Number (see the 1st column).
- Note 2.** Prob. Both = Probability in both fractions (see the 3rd column).
- Note 3. Prob. Each = Probability in each fractions (see the 8th column).
- Note 2.** Avg. = Average (see the 9th~11th, 18th~20th, and 27th~29th columns).
- Note 3.** To avoid division by zero, a value of 0.15 was substituted for CON spectral counts of 0 (see the 10th, 13th, 16th, 19th, 22th, 25th, and 28th columns) so that the EXP/CON ratios could be calculated.
- Note4.** The peptide sequences (see the 2nd column) were assorted according to Gene Symbols (see the 30th column).
- Note 5.** The peptide sequences (see the 2nd column) are only representative, since a maximum of one miscleavage may give rise to a maximum of 3 unique peptides. Therefore, only 476 different peptides were listed, though 527 unique peptides containing free cysteines were identified.
- Note 6.** Cysteins in blue (bold and underlined, see the 2nd column) were free cysteine residues, indicating they were originally S-acylated. Cysteines in red (see the 2nd column) were modified by N-ethynylmaleimide, indicating they were originally nonacylated
- Note 7.** Highly probable S-acylated peptides were highlighted with yellow (see the 2nd column).
- Note 8.** S-acylated peptides were purified from about 1.25 mg non-raft and 2.7 mg raft protein samples, respectively.

Table S6. Highly probable S-acylation sites identified by the peptide-based procedure.

Peptide	Gene Symbol	Acc. Number	Description	Sites	Known Sites	Species	Refence	Protein-based
FR C PEALFQPSFLGMES C GIHETTFNSIMK	ACTB	IPI00021439	Actin, cytoplasmic 1	272	–	Dictyostelium	16453612	
	ACTG1	IPI00021440	Actin, cytoplasmic 2	272	–	Dictyostelium	16453612	
NSGS CLCL PR	ADCY3	IPI00028513	Adenylate cyclase type 3	46/48				
C QPAPPIDEDLPEERPDD	ADORA1	IPI00026872	Adenosine A1 receptor	309	309	Human	10455026	
Y C AGEENWVDSR	ATP11A	IPI00255653	Probable phospholipid-transporting ATPase 1H	14				Highly probable
ATSV LCC LR	C13orf1	IPI00030959	24 kDa protein	7/8				Probable
MF S CVKPYEDQNYSALRR	CAPN5	IPI00643994	CDNA FLJ46245 fis, clone TESTI4020596, highly similar to Homo sapiens calpain 5	44				Probable
C FSSVSLQLSQD	CAV2	IPI00019870	Isoform Alpha of Caveolin-2	151				Probable
LG CC VVEKPQPK	CDC42SE1	IPI00024972	CDC42 small effector 1	10				
LG CC VVEKPQPK	CDC42SE1	IPI00024972	CDC42 small effector 1	11				
LG CC VVEKPQPK	CDC42SE1	IPI00024972	CDC42 small effector 1	10/11	10/11		Uniprot-probable	
SSSSSSASAAAAAASSSA S SR	CKAP4	IPI00141318	Isoform 1 of Cytoskeleton-associated protein 4	100	100	Human	18296695	Highly probable
YQEAAPNVANNTGPAA S CFGAK	CTNND1	IPI00182469	Isoform 1AB of Catenin delta-1	618				Highly probable
C SGPLGIEGGHISNQITASSTHR	EDIL3	IPI00306046	Isoform 1 of EGF-like repeat and discoidin I-like domain-containing protein 3 precursor	158				
S CGSSTPDEFPTDIPGTK	EIF2S3	IPI00297982	Eukaryotic translation initiation factor 2 subunit 3	105				
LDLPNRPETSFLWFTN C K	FER1L3	IPI00021048	Isoform 1 of Myoferlin	2013				Highly probable
AGSNMLLIGVHGPTT C EEVSMK	FLNB	IPI00289334	Isoform 1 of Filamin-B	2556				
MF F TCGPNEAMVVS G FCR	FLOT1	IPI00027438	Flotillin-1	17				Highly probable
MF F TCGPNEAMVVS G FCR	FLOT1	IPI00027438	Flotillin-1	5/17				
SPPVMVAGGRVFL P CIIQIQR	FLOT1	IPI00027438	Flotillin-1	34	34	Mouse	12370178	
DSGAALGLGIALHS P CYAQVR	G6PC3	IPI00031052	glucose-6-phosphatase catalytic subunit 3	269				
TLESMM AC CLSDEVKESK	GNA11	IPI00305551	Guanine nucleotide-binding protein subunit alpha-11	9				Highly probable
TLESMM AC CLSDEVKESK	GNA11	IPI00305551	Guanine nucleotide-binding protein subunit alpha-11	9/10	9/10	Human	9175863	
SVLSV CF PGCLLTSGEAEQQR	GNA13	IPI00290928	Guanine nucleotide-binding protein alpha-13 subunit	14				Highly probable
SVLSV CF PGCLLTSGEAEQQR	GNA13	IPI00290928	Guanine nucleotide-binding protein alpha-13 subunit	14/18	14/18/37	Human	10747909	
TLESIM AC CLSEEAKEAR	GNAQ	IPI00288947	Guanine nucleotide binding protein	10				Highly probable
TLESIM AC CLSEEAKEAR	GNAQ	IPI00288947	Guanine nucleotide binding protein	9/10	9/10	Human	8227063	
ATTVPD C CRNGLK	GPRC5A	IPI00022624	Retinoic acid-induced protein 3	9				Highly probable
QRNPMDY P VEDAF C KPQLVK	GPRC5A	IPI00022624	Retinoic acid-induced protein 3	284				
MYG C DLGPDGR	HLA-B	IPI00471955	HLA class I histocompatibility antigen, B-50 alpha chain precursor	125	332/349	Human	17785801	Highly probable
	HLA-C	IPI00473131	HLA class I histocompatibility antigen, Cw-6 alpha chain precursor	125	–	Human	17785801	Highly probable
SETVLT C ATGR	ITGA3	IPI00215995	Isoform Alpha-3A of Integrin alpha-3 precursor	904				Probable
AVVMIS C NRHTLADNFNPVSEER	M6PR	IPI00025049	Cation-dependent mannose-6-phosphate receptor precursor	145	30/34	Bovine	8647889	Highly probable
SKIVGAPMHDLLWNNATV T CHSK	MTHFD1	IPI00218342	C-1-tetrahydrofolate synthase, cytoplasmic	195				
FA C HSASLTVR	NONO	IPI00304596	Non-POU domain-containing octamer-binding protein	145				Probable
NIQTDNNSIG C FGSR	PKP2	IPI00005264	Isoform 2 of Plakophilin-2	647				
ADSERLSAP G CWA C TNFSR	PLP2	IPI00030362	Proteolipid protein 2	12/16				Probable
VYFAAEDTD C CTR	PLSCR1	IPI00005181	Phospholipid scramblase 1	148/149	184~189		12564925	Highly probable
SGAGQPLGQAAEES N CCAR	PLSCR3	IPI00216127	Phospholipid scramblase 3	125				Highly probable
SGAGQPLGQAAEES N CCAR	PLSCR3	IPI00216127	Phospholipid scramblase 3	126				

Peptide	Gene Symbol	Acc. Number	Description	Sites	Known Sites	Species	Reference	Protein-based
SGAGQPLGQAAEESN <u>CC</u> AR	PLSCR3	IPI00216127	Phospholipid scramblase 3	125/126				
VVGPCWT <u>CGC</u> GTDNTNFVK	PLSCR3	IPI00216127	Phospholipid scramblase 3	211/214/216	211/214/216		Uniprot-probable	
SLICISNEVPEHP <u>CV</u> SPVSNHVVYER	PRPF19	IPI00004968	Pre-mRNA-processing factor 19	16				Probable
ALAQEWG <u>CP</u> FMETSAK	RAP2C	IPI00009607	Ras-related protein Rap-2c precursor	140				Highly probable
HPHDIIDDINSGLV <u>CP</u> AS	RPL12	IPI00024933	60S ribosomal protein L12	162				Highly probable
AGAIAP <u>CE</u> VTVPAQNTGLGPEK	RPLP0	IPI00008530	60S acidic ribosomal protein P0	119				
ALANVNIGSL <u>C</u> NVGAGGPAPAAGAAPAGGPAPSTAAAPAEK	RPLP1	IPI00008527	60S acidic ribosomal protein P1	61				
KLLMMAGIDD <u>C</u> YTSAR	RPS2	IPI00013485	40S ribosomal protein S2	222				
MLK <u>CI</u> PLWR	SCRIB	IPI00410666	Isoform 3 of Protein LAP4	4				Highly probable
GLAAAEPTANGGLALASIEDQGAAGGY <u>C</u> GSRDQVR	SLC1A5	IPI00019472	Neutral amino acid transporter B(0)	39				Highly probable
SSGPGMAPSA <u>CCC</u> SPAALQR	SLC26A11	IPI00410334	Sulfate/anion exchanger	23/24/25				
SLNPATYIPVLPKLLSLPL <u>SC</u> QK	SLC5A6	IPI00031822	Sodium-dependent multivitamin transporter	577				Probable
G <u>CK</u> VLLNIGQQMLR	SLC7A1	IPI00027728	High-affinity cationic amino acid transporter 1	3				Highly probable
TLTELNK <u>CCGLCVCP</u> CNR	SNAP23	IPI00010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	79/80/83/85/87	80/83/85/87	Human	12551899	Highly probable
TTWGDGGENSP <u>C</u> NVVSK	SNAP23	IPI00010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	112				
GPGLFFILP <u>CT</u> DSFIK	STOM	IPI00219682	Erythrocyte band 7 integral membrane protein	87	30/87	Human	10338112	Highly probable
YRPENTPEPVSTSVSHYGAEPTTVSP <u>CP</u> SSSAK	YES1	IPI00013981	Proto-oncogene tyrosine-protein kinase Yes	42	3	Monkey	7980442	Highly probable
FRGGVNPFTNG <u>CC</u> NNVSR	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	236				Highly probable
GGVNPFTNG <u>CC</u> NNVSR	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	236/237				
VL <u>C</u> SSPAPR	ZDHHC5	IPI00328272	Isoform 1 of Probable palmitoyltransferase ZDHHC5	245				

Note 1. Acc. Number = Accession Number (see the 3rd column).

Note 2. Cysteins in blue (bold and underlined, see the 2nd column) were free cysteine residues, indicating they were originally S-acylated. Cysteines in red (see the 2nd column) were modified by N-ethylmaleimide, indicating they were originally nonacylated.

Note 3. Protein-based = Proteins also identified by using the protein-based procedure.

Table S7. Probable S-acylation sites identified by the peptide-based procedure.

Peptide	Prob. Both	Gene Symbol	Acc. Number	Description	Sites	Known Sites	Species	References	Protein-based
KCLLLLCQLR	+++	-	IPI00747966	Conserved hypothetical protein	87/92				
CQLEINFNTLQTK	++	ACTN4	IPI00013808	Alpha-actinin-4	351				
SSGCDVNLPGVNVKLPQTGISGPEIK	+++	AHNAK	IPI00555610	313 kDa protein	2572				
SCGQNPPELLPK	+++	ANLN	IPI00032958	Isoform 2 of Actin-binding protein anillin	309				
MDCSLVR	++	ATP11A	IPI00255653	Probable phospholipid-transporting ATPase IH	3				Highly probable
LIIVEGCQR	++	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	705				
NLEAVETLGSTSTCSDKTGTLTQNR	++++	ATP1A1	IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	374				
		ATP1A2	IPI00003021	Sodium/potassium-transporting ATPase alpha-1 chain precursor	372				
AGCCEWLR	++	ATP9A	IPI00024368	Isoform Long of Probable phospholipid-transporting ATPase IIA	24/25				Probable
VAQAFREGENTQVAEPEACDQMYESLAR	++	C6orf125	IPI00031617	Protein C6orf125	53				Probable
ANCFSPVSGDKPCR	++	CD38	IPI00006071	Isoform 1 of ADP-ribosyl cyclase 1	15/16				
WACLVAGGSKYSEFTSTTSGTGHNQTR	+++	CD97	IPI00299412	Isoform 2 of CD97 antigen precursor	709				
KCEPIIMTVPR	++	CORO1C	IPI00008453	coronin-1c	396				
MMCAPSATQPATAETQHIADQVR	++	CSTB	IPI00021828	Cystatin B	3				
VRPCVVYGGADIGQQIRDLER	+++	DDX3X	IPI00215637	ATP-dependent RNA helicase DDX3X	298				
QDLGGTCVNEGCIPTK	++	DERP12	IPI00382990	DERP12	45/50				
DKDDDGGEDDDANCNLICGDEYGPETR	++++	DHX9	IPI00844578	ATP-dependent RNA helicase A	608				
AITIANQTNCLPLYTK	++	DPYSL2	IPI00257508	Dihydropyrimidinase-related protein 2	248				
SSILLDVKPWDDETDMAKLEECVR	++	EEF1B2	IPI00178440	Elongation factor 1-beta	161				
CSGPGLSPGMVR	++	FLNA	IPI00302592	filamin 1	1165				
SPYTVTVGQACNPSCAR	+++	FLNA	IPI00302592	filamin 1	477/483				
VGSAADIPINISETDLSELLTATVPPSGREECELLK	+++	FLNA	IPI00302592	filamin 1	1989				
VHSPSGALEECYVTEIDQDKYAVR	++	FLNA	IPI00302592	filamin 1	2370				
YGGQPVPNFP SKLQVEPAVDTSGVCCYGP GIEGQGVFR	++	FLNA	IPI00302592	filamin 1	1260				
AHIANPSGASTE CFVTDNADGTYQVEYTPFEK	+++	FLNB	IPI00289334	Isoform 1 of Filamin-B	1280				
CLATGPGIASTVK	+++	FLNB	IPI00289334	Isoform 1 of Filamin-B	1617				
DAGYGGISLAVEGPSKVDIQTEDLEDGTCK	++	FLNB	IPI00289334	Isoform 1 of Filamin-B	2057				
GAGTGGLGLTVEGRCEAK	++	FLNB	IPI00289334	Isoform 1 of Filamin-B	1081				
SPFVVQVGEACNPNA CR	+++	FLNB	IPI00289334	Isoform 1 of Filamin-B	450				
SPFVVQVGEACNPNA CR	+++	FLNB	IPI00289334	Isoform 1 of Filamin-B	455				
SSFLVDCSKAGSNMLLIGVHGPTTCEEVSMK	++++	FLNB	IPI00289334	Isoform 1 of Filamin-B	2556			Table S6	
VAVTEGCQPSR	++	FLNB	IPI00289334	Isoform 1 of Filamin-B	1326				
VVPCLVTPVTGR	+++	FLNB	IPI00289334	Isoform 1 of Filamin-B	991				
VMSQNFTNCHTK	++	G3BP1	IPI00012442	Ras-GTPase-activating protein-binding protein 1	73				
IISNASCTTNCLAPLAK	++	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	156				
IISNASCTTNCLAPLAK	++	GAPDH	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	152/156	244	Rabbit	16128592	Highly probable
CGIFAYLNYHVP R	+++	GFPT1	IPI00217952	Isoform 1 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	2				Highly probable
CLLPAEAGGAR	++	GNA12	IPI00328744	Guanine nucleotide-binding protein alpha-12 subunit	11	11	Human	9485474	Highly probable

Peptide	Prob. Both	Gene Symbol	Acc. Number	Description	Sites	Known Sites	Species	References	Protein-based
TLESIMACCLSEEAKEAR	+++	GNAQ	IPI00288947	Guanine nucleotide binding protein	9	9/10	Human	Table S6	
LLQCDPSSASQF	+++	HPCA	IPI00219103	Neuron-specific calcium-binding protein hippocalcin	185				
VREAMCPGVSGEDSSLLLATQVEGQATNLQR	+++	JUP	IPI00554711	Junction plakoglobin	90				
MLQSLAGSSCVR	+++	KCNK1	IPI00010476	Potassium channel subfamily K member 1	10				
SFVLNLGKDSNNICLHFNPR	++++	LGALS1	IPI00219219	Galectin-1	43				Highly probable
CPEALFQPCFLGMESCIGHETTFNSIMK	++	LOC653781	IPI00479743	protein expressed in prostate, ovary, testis, and placenta 2	965/972				
CDCFHMVLPTWPGTPGSVSGR	++	LOC730269	IPI00787939	PREDICTED: similar to periaxin	2/4				
RLLYCQR	++	MMP14	IPI00218398	Matrix metalloproteinase-14 precursor	574	574	Human	15946988	Highly Probable
VASMAQSAPSEAPS CSPFGK	+++	MPP1	IPI00215610	55 kDa erythrocyte membrane protein	242	-	Human	1713685	Probable
RDWDNSGPFCTISSK	++	MPP6	IPI00303280	MAGUK p55 subfamily member 6	298	-	Human		Highly Probable
ALALAALAAVEPACGSR	++	NDFIP1	IPI00012235	Isoform 1 of NEDD4 family-interacting protein 1	15				Probable
LKGPNAVSTACTTGAHAVGDSFR	++	OXSM	IPI00016637	3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial precursor	209				
VMTIPYQMPASSPVICAGGQDR	++	PCBP1	IPI00016610	Poly(rc)-binding protein 1	194				
DLAGAPPGEVVQCFTPQSR	+++	PKP3	IPI00026952	Plakophilin-3	569				
VYFAAEDTDCCTR	++	PLSCR1	IPI00005181	Phospholipid scramblase 1	148	184~189		Table S6	
VYFAAEDTDCCTR	+++	PLSCR1	IPI00005181	Phospholipid scramblase 1	149	184~189		Table S6	
VRGPCSTYGC GSDSVFEVK	++++	PLSCR4	IPI00016776	Phospholipid scramblase 4	250/255	250/255		Uniprot-probable	
TREEECHFYAGGQVYPGEASR	+++	PRDX4	IPI00011937	Peroxiredoxin-4	51				
LLAQECACVCGWALPHNRMQALTSCECTICPD CFR	++	RNF31	IPI00094740	Isoform 1 of RING finger protein 31	702/717/719/ 722/725				
AKVDEFPLCGHMSDEYEQLSSEALEAAR	++	RPL10	IPI00554723	60S ribosomal protein L10	49				
FSVCVLGDQQHCDDEAK	++++	RPL10A	IPI00412579	60S ribosomal protein L10a	74				Probable
EYRDLTTAGAVTQC YR	++	RPL18A	IPI00026202	60S ribosomal protein L18a	109				
SACGVCPGR	++	RPL34	IPI00219160	60S ribosomal protein L34	46				
AQLNIGNVLPVGTMPGEGTIVCLEEKPGDRGK	++	RPL8	IPI00012772	60S ribosomal protein L8	114				Probable
AEPSAATQSHSISSSSFGAEPSPAGGGGGSPGACP ALGTK	+++	RTN3	IPI00028946	Reticulon-3	34				
FVQCPDGELQK	+++	RUVBL2	IPI00009104	RuvB-like 2	227				
SPAESAAAGLTCLPSVTR	+++	SFT2D3	IPI00166444	Vesicle transport protein SFT2C	67				Probable
VKVQSVETVEGCTHEVALPAEEDYLPLKPR	+++	SKIV2L2	IPI00647217	Superkiller viralicidic activity 2-like 2	110				
ACVFGNEPKASDEVPLAPR	+++	SLC35B2	IPI00384867	Isoform 2 of Adenosine 3'-phospho 5'-phosphosulfate transporter 1	80				Highly Probable
GLCFPLVK	++	SLC35B2	IPI00384867	Isoform 2 of Adenosine 3'-phospho 5'-phosphosulfate transporter 1	73				
SIGVPIKVLHEAEGHIVICTETNTGEVYR	++++	SNRPD3	IPI00017964	Small nuclear ribonucleoprotein Sm D3	10				
EAALPILEPVLGQEQAAPDQCVLFADAPEPG QALPVEEEAVTLAR	++	TNKS1BP1	IPI00304589	182 kDa tankyrase 1-binding protein	631				
CTKEEHLCTQR	+++	TPM3	IPI00178083	29 kDa protein	209				
LRCGGTAEIILDV	+++	UGCG	IPI00003861	Ceramide glucosyltransferase	384				
CVFEMPNNENDKLNMEPSK	+++	VAPA	IPI00170692	vesicle-associated membrane protein-associated protein A isoform 2	128				
MSRPSSVSPRQPAPGGGGGGGSPICPGPGGGGR	++	YTHDC2	IPI00010200	YTH domain containing 2	25				
YKVIEDYSGACCP LNK	+++	ZDHHC6	IPI00008350	Isoform 1 of Probable palmitoyltransferase ZDHHC6	328/329				Probable
GCCGNVEHVLCSPLAPR	++	ZDHHC8	IPI00385426	Isoform 1 of Probable palmitoyltransferase ZDHHC8	236/237/245				
MIPICPVVSFTYVPSRLGEDAK	+++	ZFR	IPI00333858	117 kDa protein	5				

Note 1. Acc. Number = Accession Number (see the 4rd column).

Peptide	Prob. Both	Gene Symbol	Acc. Number	Description	Sites	Known Sites	Species	References	Protein-based
---------	---------------	-------------	-------------	-------------	-------	----------------	---------	------------	---------------

Note 2. Cysteins in blue (bold and underlined, see the 1st column) were free cysteine residues, indicating they were originally S-acylated. Cysteines in red (see the 1st column) were modified by N-ethylmaleimide, indicating they were originally nonacylated.

Note 3. Protein-based = Proteins also identified by using the protein-based procedure.